

Tue Nov 2 12:23:17 2004

us-09-690-825-34\_1.rml

Page 1

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_p2n model

Run on: November 1, 2004, 18:01:56 ; Search time 85 Seconds  
(without alignments)

1187.436 Million cell updates/sec

Title: US-09-690-825-34  
Perfect score: 778  
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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

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2	778	100.0	1619	3	US-09-163-162-1 607709 Sequence 1, Appl1
3	778	100.0	1619	3	US-09-286-407-1 Sequence 1, Appl1
4	778	100.0	1619	3	US-09-496-694B-97 Sequence 97, Appl1
5	778	100.0	1619	3	US-08-448-722A-1 Sequence 1, Appl1
6	778	100.0	1619	3	US-08-189-309B-1 Sequence 1, Appl1
7	778	100.0	1619	3	US-09-016-434-918 Sequence 918, Appl1
8	778	100.0	1619	3	US-09-496-694B-10 Sequence 10, Appl1
9	778	100.0	1619	3	US-09-513-999C-2315 Sequence 2315, Appl1
10	778	100.0	1619	3	US-08-975-080-35 Sequence 35, Appl1
11	778	100.0	1619	3	US-08-630-706-10 Sequence 10, Appl1
12	778	100.0	1619	3	US-09-496-694B-3 Sequence 3, Appl1

13	246.5	31.7	624	4	US-09-738-946-3 Sequence 3, Appl1
14	244.5	31.4	665	4	US-09-270-767-10343 Sequence 10343, A
15	221	28.4	417	3	US-09-283-144-1 Sequence 1, Appl1
16	157	20.2	481	4	US-09-270-767-11886 Sequence 11886, A
17	155	19.9	5366	4	US-09-705-872-4 Sequence 4, Appl1
18	155	19.9	5502	3	US-08-836-134-1 Sequence 1, Appl1
19	155	19.9	5502	4	US-09-493-784-1 Sequence 1, Appl1
20	155	19.9	5502	4	US-09-023-655-1459 Sequence 1459, Ap
21	155	19.9	5984	4	US-09-502-582-2 Sequence 2, Appl1
22	136.5	17.5	1134	4	US-09-502-582-2 Sequence 2, Appl1
23	136.5	17.5	1337	4	US-09-127-928-1 Sequence 1, Appl1
24	136.5	17.5	1739	4	US-09-502-582-1 Sequence 1, Appl1
25	131	16.8	1559	3	US-09-239-867-1 Sequence 1, Appl1
26	131	16.8	1559	4	US-10-024-433-1 Sequence 1, Appl1
27	131	16.8	2580	2	US-08-511-485-7 Sequence 7, Appl1
28	131	16.8	2580	4	US-09-201-936-7 Sequence 7, Appl1
29	131	16.8	2580	4	US-09-011-356-7 Sequence 7, Appl1
30	131	16.8	2580	4	US-09-672-717-222 Sequence 222, App
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32	131	16.8	2589	5	US-08-569-749-1 Sequence 1, Appl1
33	131	16.8	2589	5	PCT-US96-12860-1 Sequence 1, Appl1
34	131	16.8	3532	2	US-09-205-204-1 Sequence 1, Appl1
35	131	16.8	3732	3	US-09-212-971-7 Sequence 7, Appl1
36	131	16.8	3732	3	US-08-800-929A-7 Sequence 7, Appl1
37	131	16.8	3732	3	US-09-617-053A-7 Sequence 7, Appl1
38	130	16.7	711	3	US-08-121-978-3 Sequence 3, Appl1
39	130	16.7	711	3	US-09-332-319-3 Sequence 3, Appl1
40	130	16.7	1929	4	US-09-248-786A-1277 Sequence 1277, Ap
41	129.5	16.6	2100	2	US-08-511-485-9 Sequence 9, Appl1
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44	129.5	16.6	2100	4	US-09-672-717-224 Sequence 224, App
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## ALIGNMENTS

RESULT 1  
US-09-283-144-2  
; Sequence 2, Application US/09283144  
; Patent No. 6346389  
; GENERAL INFORMATION:  
; APPLICANT: Yale University  
; TITLE OF INVENTION: Method for Selectively Modulating the Interactions  
; FILE REFERENCE: 44574-5033-US  
; CURRENT APPLICATION NUMBER: US/09/283,144  
; EARLIER FILING DATE: 1999-04-01  
; EARLIER APPLICATION NUMBER: US 60/080,288  
; EARLIER FILING DATE: 1998-04-01  
; EARLIER APPLICATION NUMBER: US 08/975,080  
; EARLIER FILING DATE: 1997-11-20  
; EARLIER APPLICATION NUMBER: PCT/US97/21860  
; EARLIER FILING DATE: 1997-11-20  
; EARLIER APPLICATION NUMBER: US 60/031,435  
; EARLIER FILING DATE: 1996-11-20  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 426  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Nucleotide sequence of open reading frame encoding  
US-09-283-144-2  
Alignment Scores:  
Pred. No.: 3.55e-93  
Score: 778.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
Length: 426  
Matches: 142  
Conservative: 0  
Mismatch: 0  
Indels: 0

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QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20  
DB 1 ATGGGTGCCCCGAGCGTTGCCCCCTGCGCCGAGCCCTTTCTCAAGAGCAACCCGATCTCT 60  
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40  
DB 61 ACATTCAAGAACTGGCCCTTTCTTGAAGGCTGCGCCCTGACCCCGAGACGAGCCGAG 120  
QY 41 AlaGlyPheIleHisCysProThrGlnAsnGluProAspLeuAlaGlnCysPhePheCys 60  
DB 121 GCTGGCTTCATCCACTGGCCCACTGAGAACGACGAGCTTGGCCGAGCTTCTTCTGTC 180  
QY 61 PheLysGluLeuGluGlyTrpGlnProAspAspProIleGluGluHisIleLysHis 80  
DB 181 TTCAAGAGCTGGAAGGCTGGAGCCAGATGACACCCCAATGAGGAACATTAAGCAT 240  
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlu 100  
DB 241 TCGTCCGGTTCGCTTCTTCTTCTGTCAGAACGAGTTTGAAGATTAACTTGTGTA 300  
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120  
DB 301 TTTTGAAGCTGACAGAGAAAGCCAGAAACAAATTGCAAGAAACCAACATTAAG 360  
QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAla 140  
DB 361 AAGAAAGATTGAGGAAACTGCGAAGAAAGTGGCCCTGCTCATGAGCAGCTGGCTGCC 420  
QY 141 MetAsp 142  
DB 421 ATGGAT 426  
RESULT 2  
US-09-163-162-1  
; Sequence 1, Application US/09163162  
; Patent No. 6077709  
; GENERAL INFORMATION:  
; APPLICANT: Bennett, C. Frank  
; APPLICANT: Ackermann, Elizabeth J.  
; APPLICANT: Swayze, Eric E.  
; APPLICANT: Cowsett, Lex M.  
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION  
; FILE REFERENCE: RUS-0008  
; CURRENT APPLICATION NUMBER: US/09/163,162  
; CURRENT FILING DATE: 1998-09-29  
; NUMBER OF SEQ ID NOS: 47  
; SEQ ID NO 1  
; LENGTH: 1619  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (50)..(478)  
US-09-163-162-1  
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Score: 778.00 Matches: 142  
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Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
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QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20  
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QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40  
DB 110 ACATTCAAGAACTGGCCCTTTCTTGAAGGCTGCGCCCTGACCCCGAGCGAGTGCCGAG 169  
QY 41 AlaGlyPheIleHisCysProThrGlnAsnGluProAspLeuAlaGlnCysPhePheCys 60  
DB 170 GCTGGCTTCATCCACTGGCCCACTGAGAACGAGCACTTGGCCGAGCTTCTTCTGTC 229  
QY 61 PheLysGluLeuGluGlyTrpGlnProAspAspProIleGluGluHisIleLysHis 80  
DB 230 TTCAAGAGCTGGAAGGCTGGAGCCAGATGACGCCCAATGAGGAACATTAAGCAT 289  
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlu 100  
DB 290 TCGTCCGGTTCGCTTCTTCTTCTGTCAGAACGAGTTTGAAGATTAACTTGTGTA 349  
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120  
DB 350 TTTTGAAGCTGACAGAGAAAGCCAGAAACAAATTGCAAGAAACCAACATTAAG 409  
QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAla 140  
DB 410 AAGAAAGATTGAGGAAACTGCGAAGAAAGTGGCCCTGCTCATGAGCAGCTGGCTGCC 469  
QY 141 MetAsp 142  
DB 470 ATGGAT 475  
RESULT 3  
US-09-286-407-1  
; Sequence 1, Application US/09286407A  
; Patent No. 6165788  
; GENERAL INFORMATION:  
; APPLICANT: Bennett, C. Frank  
; APPLICANT: Ackermann, Elizabeth J.  
; APPLICANT: Swayze, Eric E.  
; APPLICANT: Cowsett, Lex M.  
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION  
; FILE REFERENCE: ISPH-0345  
; CURRENT APPLICATION NUMBER: US/09/286,407A  
; CURRENT FILING DATE: 1999-04-05  
; NUMBER OF SEQ ID NOS: 48  
; SEQ ID NO 1  
; LENGTH: 1619  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (50)..(478)  
US-09-286-407-1  
Alignment Scores:  
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Score: 778.00 Matches: 142  
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Query Match: 100.00% Indels: 0  
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QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40  
DB 110 ACATTCAAGAACTGGCCCTTTCTTGAAGGCTGCGCCCTGACCCCGAGCGAGCCGAG 169  
QY 41 AlaGlyPheIleHisCysProThrGlnAsnGluProAspLeuAlaGlnCysPhePheCys 60  
DB 170 GCTGGCTTCATCCACTGGCCCACTGAGAACGAGCACTTGGCCGAGCTTCTTCTGTC 229

QY 61 PheLeuLysLeuAspArgGluThrAlaLysAsnLysIleAlaLysGluThrAsnLys 80  
DB 230 TTCACGAGCTGGACAGCTGGAGCGACGATGACGACCCATGAGAACATTAAGAGCAT 289  
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGluPheGluGluLeuThrLeuGluGlu 100  
DB 290 TCGTCCGCTGGCTTCT 349  
QY 101 PheLeuLysLeuAspArgGluThrAlaLysAsnLysIleAlaLysGluThrAsnLys 120  
DB 350 TTTTGAACCTGACAGAGAAAGCCCAAGAACAAATTGCAAGAGAAACCAACATTAAG 409  
QY 121 LysLysGluPheGluGluThrAlaLysLysValArgAlaIleGluGluLeuAla 140  
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QY 141 MetAsp 142  
DB 470 ATGAT 475  
RESULT 4  
US-09-496-694B-97  
; Sequence 97, Application US/09496694B  
; Patent No. 6335194  
; GENERAL INFORMATION:  
; APPLICANT: C. Frank Bennett  
; APPLICANT: Elizabeth J. Ackermann  
; APPLICANT: Eric B. Swartz  
; APPLICANT: Lex M. Cowsett  
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION  
; FILE REFERENCE: ISPH-0439  
; CURRENT APPLICATION NUMBER: US/09/496,694B  
; PRIORITY FILING DATE: 2000-02-02  
; PRIOR APPLICATION NUMBER: 09/286,407  
; PRIORITY FILING DATE: 1999-04-05  
; PRIOR APPLICATION NUMBER: 09/163,162  
; PRIORITY FILING DATE: 1998-09-29  
; NUMBER OF SEQ ID NOS: 249  
; SEQ ID NO 97  
; LENGTH: 1619  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-496-694B-97  
Alignment Scores:  
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Score: 778.00 Matches: 142  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0  
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QY 1 MetGlyAlaProThrLeuProProAlaITrGlnProPheLeuLysAspHsArgIleSer 20  
DB 50 ATGGGTGCCCCGAGCTGGCCCCCTGCTGGACCCCTTCTCAAGACCAACCCGACCTCT 109  
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40  
DB 110 ACATTCAGAACTGGCCCTCTTGGAGGCTGGCGCTGCAACCCCGAGCGGAGTGGCGAG 169  
QY 41 AlAGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGluCysPhePheCys 60  
DB 170 GCTGGCTTCACTCCCTCCACACTGAGAACGAGCCGACTTGGCCCACTGTTCTTCTG 229  
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspAspProIleGluGluHisLysLysHis 80  
DB 230 TTCAGAGCTGGAAGCTGGAGCCGATGACGACCCCATTAAGAACTTAAGAAAGCAT 289  
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGluPheGluGluLeuThrLeuGluGlu 100  
DB 290 TCGTCCGCTGGCTTCT 349

QY 101 PheLeuLysLeuAspArgGluThrAlaLysAsnLysIleAlaLysGluThrAsnLys 120  
DB 350 TTTTGAACCTGACAGAGAAAGCCCAAGAACAAATTGCAAGAGAAACCAACATTAAG 409  
QY 121 LysLysGluPheGluGluThrAlaLysLysValArgAlaIleGluGluLeuAla 140  
DB 410 AAGAAAGATTGAGAGAACTGCGAAGAAAGTGGCCCTGCTCAGTGGCTGCC 469  
QY 141 MetAsp 142  
DB 470 ATGAT 475  
RESULT 5  
US-08-448-722A-1/c  
; Sequence 1, Application US/08448722A  
; Patent No. 6072028  
; GENERAL INFORMATION:  
; APPLICANT: Altieri, Dario C.  
; TITLE OF INVENTION: No. 6072028e1 Cell Surface Receptor, Antibody  
; TITLE OF INVENTION: Compositions, and Methods of Using Same  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Office of Patent Counsel, The Scripps  
; ADDRESS: Research Institute  
; STREET: 10550 No. 6072028th Torrey Pines Road, TPC-8  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: US  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/448,722A  
; FILING DATE: 25-MAY-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/189,309  
; FILING DATE: 28-JAN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitting, Thomas  
; REGISTRATION NUMBER: 34,163  
; REFERENCE/DOCKET NUMBER: 233.1 Div1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 784-2937  
; TELEFAX: (619) 784-9399  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1165 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 37..1047  
US-08-448-722A-1  
Alignment Scores:  
Pred. No.: 1,42e-88 Length: 1165  
Score: 748.00 Matches: 140  
Percent Similarity: 99.30% Conservative: 1  
Best Local Similarity: 98.59% Mismatches: 1  
Query Match: 96.14% Indels: 1  
DB: 3 Gaps: 0  
US-09-690-825-34 (1-142) x US-08-448-722A-1 (1-1165)

QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20  
DB 1114 ATGGGTGCCCCGAGCTGCCCCCTGCTGGCAGGCCCTTTCTCAAGAGCCACCGCATCTCT 1055  
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40  
DB 1054 ACATTCAAGAACTGGCCCTTTCTTGGAGGGCTGCC -TGCACCCCGGAGCGGATGGCCGAG 996  
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60  
DB 995 GCTGGCTTCATCCACTGCCCCACGAGAGCAAGCACTTGGCCCATGTTCTTCTGTC 936  
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluIleHisLysLysHis 80  
DB 935 TTCAAGAGCTGGAAGCTGGAGCCGAGATGACACCCCATAGAGAACTATAAAAGCAT 876  
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluLeuThrLeuGlyGlu 100  
DB 875 TCGTCCGGTTCGCTTCTTCTGTCAGAGCAGATTGAAGATTAACTTGGTGA 816  
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120  
DB 815 TTTTGAACCTGCAAGAGAAAGCCAGAACAAATTGCAAGAAACCAATTAAG 756  
QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAla 140  
DB 755 AAGAAAGATTGAGAAACTGCGAAGAAAGTGGCGCTGCATCGAGCGCTGGCTCG 696  
QY 141 MetAsp 142  
DB 695 ATGGAT 690

RESULT 6  
US-08-189-309B-1/c  
Sequence 1, Application US/08189309B  
Patent No. 6238875

GENERAL INFORMATION:

APPLICANT: Altermir, Dario C.

TITLE OF INVENTION: Diagnostic Methods Useful in the Characterization of

TITLE OF INVENTION: Lymphoproliferative Disease Characterized by Increased EPR-1

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Office of Patent Counsel, The Scripps

STREET: 10550 No. 6238875th Torrey Pines Road, TPC-8

CITY: La Jolla

STATE: CA

COUNTRY: US

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/189,309B

FILING DATE: 28-JAN-1994

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/988,897

FILING DATE: 10-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/667,957

FILING DATE: 12-MAR-1991

ATTORNEY/AGENT INFORMATION:

NAME: Fitting, Thomas

REGISTRATION NUMBER: 34,163

REFERENCE/DOCKET NUMBER: 233.1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 784-2937

TELEFAX: (619) 784-9399

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1165 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 37..1047  
US-08-189-309B-1

Alignment Scores:  
Pred. No.: 1,42e-88 Length: 1165  
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Best Local Similarity: 98.59% Mismatches: 1  
Query Match: 96.14% Indels: 1  
DB: 3 Gaps: 0

US-09-690-825-34 (1-142) x US-08-189-309B-1 (1-1165)

QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20  
DB 1114 ATGGGTGCCCCGAGCTGCCCCCTGCTGGCAGGCCCTTTCTCAAGAGCCACCGCATCTCT 1055  
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40  
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DB 995 GCTGGCTTCATCCACTGCCCCACGAGAGCAAGCACTTGGCCCATGTTCTTCTGTC 936  
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluIleHisLysLysHis 80  
DB 935 TTCAAGAGCTGGAAGCTGGAGCCGAGATGACACCCCATAGAGAACTATAAAAGCAT 876  
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluLeuThrLeuGlyGlu 100  
DB 875 TCGTCCGGTTCGCTTCTTCTGTCAGAGCAGATTGAAGATTAACTTGGTGA 816  
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120  
DB 815 TTTTGAACCTGCAAGAGAAAGCCAGAACAAATTGCAAGAAACCAATTAAG 756  
QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAla 140  
DB 755 AAGAAAGATTGAGAAACTGCGAAGAAAGTGGCGCTGCATCGAGCGCTGGCTCG 696  
QY 141 MetAsp 142  
DB 695 ATGGAT 690

RESULT 7  
US-09-016-434-918

Sequence 918, Application US/09016434  
Patent No. 650938

GENERAL INFORMATION:

APPLICANT: Janice Au-Young

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

TITLE OF INVENTION: PATHWAY GENE EXPRESSION

NUMBER OF SEQUENCES: 1490

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/016,434  
FILING DATE: HEREWITH  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0002 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 918:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 740 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: BRAIT0701  
CLONE: 752848  
US-09-016-434-918

Alignment Scores:  
Pred. No.: 2,55e-85 Length: 740  
Score: 721.00 Matches: 135  
Percent Similarity: 95.74% Conservative: 0  
Best Local Similarity: 95.74% Mismatches: 6  
Query Match: 92.67% Indels: 1  
Gaps: 0

US-09-690-825-34 (1-142) x US-09-016-434-918 (1-740)

QY 2 G1YAlaProThrLeuProAlaTrpGlnProPheLeuLysAspHisArgIleSerThr 21  
Db 22 GGGGCGCNCNGCTGGCCACT-GCCTGGCCTCCCTTCTCAAGACCGCATCTCTACA 80

QY 22 PheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGluAla 41  
Db 81 TTCAAGAACTGGCCCTCTTGGAGGGCTGGCTGCACCCCGAGGGAGTGGCGAGGCT 140

QY 42 G1YPheIleHisCysProThrGluAsnGluProAspLeuIleGlnCysPhePheCysPhe 61  
Db 141 GGCTTCATCCACTGCCCACTGAMAAAGACGACACTGGCCCAAGTCTTCTCTCTTC 200

QY 62 LysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysSer 81  
Db 201 AAGGAGCTGAAGGCTGGAGCCGATGACGACCCCTAAGAGAACTAAAGCAATTG 260

QY 82 SerGlyCysAlaPheLeuSerValLysGlnPheGluLeuThrLeuGluGluPhe 101  
Db 261 TCCGCTTGGCTTCT 320

QY 102 LeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 121  
Db 321 TTGAAACTGACAGAAAGAGCCAAAGACAAATTCAGAAAGAAACCAATTAAGAAG 380

QY 122 LysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGluLeuAlaMet 141  
Db 381 AAAAGAAATTTGAGAACTGCAAGAAAGTGGCGCTCCATCGAGCGCTGGCTGCCATG 440

QY 142 Asp 142  
Db 441 GAT 443

RESULT 8  
US-09-496-694B-10

Sequence 10, Application US/09496694B  
Patent No. 6335194  
GENERAL INFORMATION:  
APPLICANT: C. Frank Bennett  
APPLICANT: Elizabeth J. Ackermann  
APPLICANT: Eric B. Swartz  
APPLICANT: Lex M. Cowser  
TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION  
FILE REFERENCE: ISPH-0439  
CURRENT APPLICATION NUMBER: US/09/496,694B  
CURRENT FILING DATE: 2000-02-02  
PRIOR APPLICATION NUMBER: 09/286,407  
PRIOR FILING DATE: 1999-04-05  
PRIOR APPLICATION NUMBER: 09/163,162  
PRIOR FILING DATE: 1998-09-29  
NUMBER OF SEQ ID NOS: 249  
SEQ ID NO 10  
LENGTH: 955  
TYPE: DNA  
ORGANISM: Mus musculus  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (109)...(531)  
US-09-496-694B-10

Alignment Scores:  
Pred. No.: 3,95e-77 Length: 955  
Score: 660.00 Matches: 118  
Percent Similarity: 92.66% Conservative: 12  
Best Local Similarity: 84.29% Mismatches: 10  
Query Match: 84.83% Indels: 0  
Gaps: 0

US-09-690-825-34 (1-142) x US-09-496-694B-10 (1-955)

QY 1 MetGlyAlaProThrLeuProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20  
Db 109 ATGGAGCTCCGGCCCTCCCAAGATCTGGCAGCTGTCTCTCAAGAACTACCGATGCC 168

QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40  
Db 169 ACCTTCAGAACTGGCCCTCTCTGAGAGACTGGCGCTGCACCCAGAGCGAATGGCGAG 228

QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuIleGlnCysPhePheCys 60  
Db 229 GCTGGCTTCATCCACTGCCCTTACCAAGACGAGCTGATTTGGCCAGTCTTTTCTGC 288

QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis 80  
Db 289 TTTAAGAAATTTGAAGAGCTGGGAACCGATGACAAACCGATAGAGACATAGAAAGAC 348

QY 81 SerSerGlyCysAlaPheLeuSerValLysGlnPheGluLeuThrLeuGluGlu 100  
Db 349 TCCCTGGCTGGCTTCT 408

QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120  
Db 409 TTCTTGAACCTGACAGACAGACGAGCCAAAGACAAATTCAGAAAGAAACCAATTAAGAAG 468

QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGluLeuAlaMet 140  
Db 469 CAAAAGAGTTTGAAGAGACTGCAAGAACTACCCGCTCAGTCAATTCAGACAGCTGCC 528

RESULT 9  
US-09-513-999C-2315  
Sequence 2315, Application US/09513999C  
Patent No. 6783961  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Ducaslet, A.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
Patent No. 6783961

FILE REFERENCE: 59. US2.REG  
CURRENT APPLICATION NUMBER: US/09/513.999C  
CURRENT FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/122,487  
PRIOR FILING DATE: 1999-02-26  
NUMBER OF SEQ ID NOS: 36681  
SOFTWARE: Patent.pm  
SEQ ID NO 2315  
LENGTH: 399  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 52..399  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 32  
OTHER INFORMATION: k=g or t  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 279  
OTHER INFORMATION: r=a or g  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 280  
OTHER INFORMATION: s=g or c  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 318  
OTHER INFORMATION: s=g or c  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 342  
OTHER INFORMATION: s=g or c  
FEATURE:  
NAME/KEY: UNSURE  
LOCATION: 77  
OTHER INFORMATION: Xaa=asp or His  
US-09-513-999C-2315

Alignment Scores:  
Pred. No.: 2,47e-75 Length: 399  
Score: 642.00 Matches: 115  
Percent Similarity: 99.14% Conservative: 0  
Best Local Similarity: 99.14% Mismatches: 1  
Query Match: 82.52% Indels: 0  
DB: Gaps: 0

US-09-690-825-34 (1-142) x US-09-513-999C-2315 (1-399)  
QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuYsaPhtsArgIleSer 20  
DB 52 ATGGGTGCCCCGACGCTTGGCCCTGCGCAGCCCTTTCTCAAGACCCACCATCTCT 111  
QY 21 ThrPheLeuYsaAntTPProPheLeuGluGlyCysAlaCysThrProGluuArgMetAlaGlu 40  
DB 112 ACATTCAAGAACTGGCCCTTCTTGGAGGCGCTGCGCCCTGCAACCCGAGCGAGTGGCCGAG 171  
QY 41 AlaGlyPheIleHtHsCysProThrGluAsnGluProAspLeuIaGlnCysPhePheCys 60  
DB 172 GCTGGCTTCATCCACTGCCCCCAGTGAAGACGACCACTTGGCCCACTTTCTTCTCTG 231  
QY 61 PheLeuGluLeuGluGlyTrpGluProAspAspAspProIleGluuHtHsIleSlySHs 80  
DB 232 TTCAAGAGAGCTGGAAGGCTGGGAGCCAGATGACGACCCCATAGAGGARSATATAAAGCAT 291  
QY 81 SerGerglyCysAlaPheLeuSerValIleYsLeuGlnPheGluGluLeuThrLeuGluYglu 100  
DB 292 TCGTCGGGTGGCGCTTCTTCTTCTGTSAAAGAGCAGTTTGAAGATTAACSTTGGTGA 351  
QY 101 PheLeuYsLeuAspArgIuArgAlaYsaHtHsIleAlaYsGlu 116  
DB 352 TTTTGAAGCTGACAGAGAAAGGCCAAGAACAAATTCACAAGGA 399

RESULT 10  
US-08-975-080-35  
Sequence 35, Application US/08975080  
Patent No. 6245523  
GENERAL INFORMATION:  
APPLICANT: Allier, Dario C.  
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS  
NUMBER OF INVENTION: CELLULAR APOPTOSIS, AND ITS MODULATION  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP  
STREET: 1900 M Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20036-5869  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/975,080  
FILING DATE: 20-NOV-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/031,435  
FILING DATE: 20-NOV-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Adler, Reid G.  
REGISTRATION NUMBER: 30,988  
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-467-7000  
TELEFAX: 202-467-7176  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14796 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-975-080-35

Alignment Scores:  
Pred. No.: 8.89e-39 Length: 14796  
Score: 382.00 Matches: 73  
Percent Similarity: 46.84% Conservative: 1  
Best Local Similarity: 46.20% Mismatches: 0  
Query Match: 49.10% Indels: 84  
DB: Gaps: 1

US-09-690-825-34 (1-142) x US-08-975-080-35 (1-14796)  
QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuYsaPhtsArgIleSer 20  
DB 2811 ATGGGTGCCCCGACGCTTGGCCCTGCGCAGCCCTTTCTCAAGACCCACCATCTCT 2870  
QY 21 ThrPheLeuYsaAntTPProPheLeuGluGlyCysAlaCysThrProGluuArg- 37  
DB 2871 ACATTCAAGAACTGGCCCTTCTTGGAGGCGCTGCGCCCTGCAACCCGAGCGGTAGACTG 2930  
QY 37 ----- 37  
DB 2931 CCCGCTCTGAGGTCGCCGCCACCGCGCTTGGCTGCTGCTTACGAGGACCACTGTGAC 2990  
QY 37 ----- 37  
DB 2991 TGGGCTTGAGGAGTCAAGCCGCTTCCCTCCCTGCTGTCTCCCAAGAGGCACTGT 3050  
QY 37 ----- 37  
DB 3051 GGCTGGCCCTTGGGTCCAGGCGGCGCTCCCTCCTGCTTGTCTTCCCATGAGGCTT 3110

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QY 37 ----- 37
Db 3111 TGTGGCTGGGCTTCGGGGCTTCGGGCTGCACGCTCCAGCTGTCGTCCTG 3170
QY 38 ---MetAgluaIaGlyPheIIeHisCysProTh-GluAsnGluProAspLeuAlaGln 56
Db 3171 CAGATGGCCCGAGGCTGGCTTCATCCACTGCCCCACAGAGACGAGCAGACTTGCGCCAG 3230
QY 57 CysPhePheCysPheGluLeuGluGlyTyrGluProAspAspAspProile 74
Db 3231 TGTTCCTTCCTTCAGAGAGCTGGAGGCTGGAGGCTGAGAGCCAGATGACACCCCATG 3284

RESULT 11
US-09-630-706-10
; Sequence 10, Application US/09630706
; Patent No. 6277640
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF HER-3 EXPRESSION
; FILE REFERENCE: RTS-0053
; CURRENT APPLICATION NUMBER: US/09/630, 706
; CURRENT FILING DATE: 2000-08-01
; NUMBER OF SEQ ID NOS: 94
; SEQ ID NO 10
; LENGTH: 14796
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2811)...(2921)
; NAME/KEY: CDS
; LOCATION: (3174)...(3283)
; NAME/KEY: CDS
; LOCATION: (5158)...(5275)
; NAME/KEY: CDS
; LOCATION: (11955)...(12044)
US-09-630-706-10

Alignment Scores:
Pred. No.: 8.89e-39 Length: 14796
Score: 382.00 Matches: 73
Percent Similarity: 46.84% Conservative: 1
Best Local Similarity: 46.20% Mismatches: 0
Query Match: 49.10% Indels: 84
DB: 3 Gaps: 1

US-09-690-825-34 (1-142) x US-09-630-706-10 (1-14796)
QY 1 MetGlyAlaProThrLeuProProAlaTyrGlnProPheLeuLysAspHisArgIleSer 20
Db 2811 ATGGGTGCCCCGAGCTGGCCCCCTGCTGGCAGGCCCTTTCTCAAGAGACCGCATCTCT 2870
QY 21 ThrPheLysAsnTyrProPheLeuGluGlyCysAlaCysThrProGluArg 37
Db 2871 ACATTCAAGAACTGGCCCTTCTTGAGAGGCTGGCGCTGCACCCCGAGCGGGTGAAGACTG 2930
QY 37 ----- 37
Db 2931 CCGGGCTCTGGAGGTCCCGCCAGCCCGCTTGCTCCCTAGAGAGCCACTGTGAC 2990
QY 37 ----- 37
Db 2991 TGGGCTCGGGGGATACAGCCGCCCTCCCTCCCGCTGTCGCCAGAGGCCACTGT 3050
QY 37 ----- 37
Db 3051 GAGTGGCCCTTGGGTCCAGGCGGCTCCCTCCCTGTTGTGCCATGAGGCTT 3110
QY 37 ----- 37
Db 3111 TGTGGCTGGGCTTCGGGGTTCGGGCTGCACGTCACATCAGAGCTGTGCTGCTTG 3170
```

```
QY 38 ---MetAgluaIaGlyPheIIeHisCysProThGluAsnGluProAspLeuAlaGln 56
Db 3171 CAGATGGCCCGAGGCTGGCTTCATCCACTGCCCCACAGAGACGAGCAGACTTGCGCCAG 3230
QY 57 CysPhePheCysPheGluLeuGluGlyTyrGluProAspAspAspProile 74
Db 3231 TGTTCCTTCCTTCAGAGAGCTGGAGGCTGGAGGCTGAGAGCCAGATGACACCCCATG 3284

RESULT 12
US-09-496-694B-3
; Sequence 3, Application US/09496694B
; Patent No. 6335194
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Eric E. Swazy
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: ISPH-0439
; CURRENT APPLICATION NUMBER: US/09/496, 694B
; PRIOR FILING DATE: 2000-02-02
; PRIOR APPLICATION NUMBER: 09/286, 407
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 09/163, 162
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 249
; SEQ ID NO 3
; LENGTH: 14796
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2811)...(2921)
; NAME/KEY: CDS
; LOCATION: (3174)...(3283)
; NAME/KEY: CDS
; LOCATION: (5158)...(5275)
; NAME/KEY: CDS
; LOCATION: (11955)...(12044)
US-09-496-694B-3

Alignment Scores:
Pred. No.: 8.89e-39 Length: 14796
Score: 382.00 Matches: 73
Percent Similarity: 46.84% Conservative: 1
Best Local Similarity: 46.20% Mismatches: 0
Query Match: 49.10% Indels: 84
DB: 3 Gaps: 1

US-09-690-825-34 (1-142) x US-09-496-694B-3 (1-14796)
QY 1 MetGlyAlaProThrLeuProProAlaTyrGlnProPheLeuLysAspHisArgIleSer 20
Db 2811 ATGGGTGCCCCGAGCTGGCCCCCTGCTGGCAGGCCCTTTCTCAAGAGACCGCATCTCT 2870
QY 21 ThrPheLysAsnTyrProPheLeuGluGlyCysAlaCysThrProGluArg 37
Db 2871 ACATTCAAGAACTGGCCCTTCTTGAGAGGCTGGCGCTGCACCCCGAGCGGGTGAAGACTG 2930
QY 37 ----- 37
Db 2931 CCGGGCTCTGGAGGTCCCGCCAGCCCGCTTGCTCCCTAGAGAGCCACTGTGAC 2990
QY 37 ----- 37
Db 2991 TGGGCTCGGGGGATACAGCCGCCCTCCCTCCCGCTGTCGCCAGAGGCCACTGT 3050
QY 37 ----- 37
Db 3051 GAGTGGCCCTTGGGTCCAGGCGGCTCCCTCCCTGTTGTGCCATGAGGCTT 3110
QY 37 ----- 37
```

```
Db 3111 TGTGGCTGGGCGCTCGGGGTTCCGGGCTGCCACGTCACGAGCTGTGTCCTTG 3170
Qy 38 ---MetAlaGluAlaGlyPheIleHisCysProThrGluSerGluProAlaGln 56
Db 3171 CAGATGGCGGAGGCTGGCTGCTTATCCACTGCCCTCAGAACGAGCGACCTGGCCGAG 3230
Qy 57 CysPhePheCysPheGluLeuGluGlyTyrGluProAspAspPhePhe 74
Db 3231 TGTTCCTTCCTTCCTTCAGAGAGCTGGAAAGCTGGAGCCAGCATGACGCCACCA 3284

RESULT 13
US-09-738-946-3
; Sequence 3, Application US/09738946
; Patent No. 6579701
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: DROSOPHILA HOMOLOGUES OF GENES AND PROTEINS IMPLICATED IN CANCER
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: EX00-043C
; CURRENT APPLICATION NUMBER: US/09/738,946
; CURRENT FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 60/170,832
; PRIOR FILING DATE: 1999-12-14
; PRIOR APPLICATION NUMBER: 60/170,838
; PRIOR FILING DATE: 1999-12-14
; PRIOR APPLICATION NUMBER: 60/178,580
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/185,879
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/185,880
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/186,150
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/189,701
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 624
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-738-946-3

Alignment Scores:
Pred. No.: 5,01e-23 Length: 624
Score: 246.50 Matches: 48
Percent Similarity: 57.14% Conservative: 20
Best Local Similarity: 40.34% Mismatches: 50
Query Match: 31.68% Indels: 1
Gaps: 1

US-09-690-825-34 (1-142) x US-09-738-946-3 (1-624)
Qy 14 LeuLysAspHisArgIleSerThrPheLysAsnTyrProPheLeuGluGlyCysAlaCys 33
Db 139 CTGGAACAGCATCGCGTGAAGAGCTACAGAGTTGGCCCTTCGAGAGCCGATCTCG 198
Qy 34 ThrProGluArgMetAlaGluAlaGlyPheIleHisCysProThrGluSerGluProAsp 53
Db 199 AGCATTTGGAAGAGCGCGGAGCGGATTCATTGACCGGACCAAGCGGAAACGAC 258
Qy 54 LeuAlaGlnCysPhePheCysPheGluLeuGluGlyTyrGluProAspAspPhePhe 73
Db 259 ACTGCCACTTGTTCCTGCTGGGAAAGACCTCGATGCTGGAGCCCGAAGATGATCCG 318
Qy 74 IleGluGluHisLysLysHisSerSerGlyCysAlaPheLeuSerValLysGlnPhe 93
Db 319 TGGAGAGAGCACCGTGAACATGACCCCAATGCGAGTTCCCAAGCTATGTCGCCGA 378
Qy 94 GluGluLeuThrLeuGluGluPheLeuLysLeuAspArgGluArgAlaLysAsnLysIle 113
Db 379 AGGAATTAAACCGATACCAATTTCCTGGAATTCCTTGGAACCGTCTTAAGCAGACATA 438
```

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Qy 114 AlaLysGluThrAsnAsnLysLysLysGluPhe---GluGluThrAlaLysLysVal 131
Db 439 GAGAAACCTGCAAAAGCCTTCAATCGAGCTTCCTGCGGAGATGAGAGCGCTTA 495

RESULT 14
US-09-270-767-10343
; Sequence 10343, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10343
; LENGTH: 665
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-10343

Alignment Scores:
Pred. No.: 1,01e-22 Length: 665
Score: 244.50 Matches: 48
Percent Similarity: 56.30% Conservative: 19
Best Local Similarity: 40.34% Mismatches: 51
Query Match: 31.43% Indels: 1
Gaps: 1

US-09-690-825-34 (1-142) x US-09-270-767-10343 (1-665)
Qy 14 LeuLysAspHisArgIleSerThrPheLysAsnTyrProPheLeuGluGlyCysAlaCys 33
Db 182 CTGGAACAGCATCGCGTGAAGAGCTACAGAGTTGGCCCTTCGAGAGCCGATCTCG 241
Qy 34 ThrProGluArgMetAlaGluAlaGlyPheIleHisCysProThrGluSerGluProAsp 53
Db 242 AGCATTTGGAAGAGCGCGGAGCGGATTCATTGACCGGACCAAGCGGAAACGAC 301
Qy 54 LeuAlaGlnCysPhePheCysPheGluLeuGluGlyTyrGluProAspAspPhePhe 73
Db 302 ACTGCCACTTGTTCCTGCTGGGAAAGACCTCGATGCTGGAGCCCGAAGATGATCCG 361
Qy 74 IleGluGluHisLysLysHisSerSerGlyCysAlaPheLeuSerValLysGlnPhe 93
Db 362 TGGAGAGAGCACCGTGAACATGACCCCAATGCGAGTTCCCAAGCTATGTCGCCGA 421
Qy 94 GluGluLeuThrLeuGluGluPheLeuLysLeuAspArgGluArgAlaLysAsnLysIle 113
Db 422 AGGAATTAAACCGATACCAATTTCCTGGAATTCCTTGGAACCGTCTTAAGCAGACATA 481
Qy 114 AlaLysGluThrAsnAsnLysLysLysGluPhe---GluGluThrAlaLysLysVal 131
Db 482 GAAAAACCTGCAAAAGCCTTCAATCGAGCTTCCTGCGGAGATGAGAGCGCTTA 538

RESULT 15
US-09-283-144-1
; Sequence 1, Application US/09283144
; Patent No. 6346389
; GENERAL INFORMATION:
; APPLICANT: Yale University
; TITLE OF INVENTION: Method for selectively Modulating the Interactions
; TITLE OF INVENTION: between Survivin and Tubulin
; FILE REFERENCE: 44574-5033-US
; CURRENT APPLICATION NUMBER: US/09/283,144
; CURRENT FILING DATE: 1999-04-01
; EARLIER APPLICATION NUMBER: US 60/080,288
; EARLIER FILING DATE: 1998-04-01
; EARLIER APPLICATION NUMBER: US 08/975,080
; EARLIER FILING DATE: 1997-11-20
; EARLIER APPLICATION NUMBER: PCT/US97/21880
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; EARLIER FILING DATE: 1997-11-20  
; EARLIER APPLICATION NUMBER: US 60/031,435  
; EARLIER FILING DATE: 1996-11-20  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 1  
; LENGTH: 417  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: DNA sequence of proximal 5' flanking region of  
; OTHER INFORMATION: Survivin gene  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (291)..(401)  
US-09-283-144-1

Alignment Scores:  
Pred. No.: 6,16e-20 Length: 417  
Score: 221.00 Matches: 38  
Percent Similarity: 92.86% Conservative: 1  
Best Local Similarity: 90.48% Mismatches: 3  
Query Match: 28.41% Indels: 0  
DB: 3 Gaps: 0

US-09-690-825-34 (1-142) X US-09-283-144-1 (1-417)

QY 1 MetGlyAlaProThrLeuProPheAlaTTPGlnProPheLeuLysAspHisArgIleSer 20  
Db 291 ATGGTGGCCCCGCGCGTGGCCCCCTGGCGACGCCCTTCTCAAGGACCCCGCATCTCT 350  
QY 21 ThrPheLysAsnTrpProPheLeuGlnGlyCysAlaCysThrProGluArgMetAlaGlu 40  
Db 351 ACATTCAAGACTGGCCCTTCTTGGAGGCGCTGGCGCTGCACCCCGAGCGGCTGAGACTG 410  
QY 41 AlaGly 42  
Db 411 CCCGGC 416

Search completed: November 1, 2004, 19:18:42  
Job time: 100 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame\_plus.p2n model

Run on: November 1, 2004, 20:31:52 ; Search time 369 Seconds  
(without alignments)  
1973.223 Million cell updates/sec

Title: US-09-690-825-34

Perfect score: 142

Sequence: 1 MGAAPTLPAMQPLKDRHS.....EPETAKYRAIEDLAMD 142

Scoring table:

Oligo	Xgapop 60.0	Xgapext 60.0
Ygapop 60.0	Ygapext 60.0	Fgapop 6.0
Delop 6.0	Delext 7.0	

Searched: 3413475 seqs, 256380928 residues

Word size: 1

Total number of hits satisfying chosen parameters: 6817622

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Command line parameters:

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-Q=/cgn2\_1/USPTO.spool.p/US09690825/runat\_0112004\_105500\_2117/app.query.fasta.1.327  
-DB=Published.Applications.NA -QFMT=fastcap -SUFFIX=rmpb -MIMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=equality -THR MIN=1  
-ALIGN=15 -MODE=IOCL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=200000000 -USER=US09690825@cgn\_1.1.723@runat\_0112004\_105500\_2117  
-NCPU=6 -ICPU=3 -NO\_MMAP -JARBQUERY -NEG\_SCORES=0 -WAIT -DSBLOCX=100  
-LONGLOG -DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database:

Published Applications NA:

- 1: /cgn2\_6/prodata/1/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/prodata/1/pubpna/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/prodata/1/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/prodata/1/pubpna/US07\_PUBCOMB.seq.\*
- 5: /cgn2\_6/prodata/1/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/prodata/1/pubpna/PCTUS\_PUBCOMB.seq.\*
- 7: /cgn2\_6/prodata/1/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/prodata/1/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/prodata/1/pubpna/US09\_PUBCOMB.seq.\*
- 10: /cgn2\_6/prodata/1/pubpna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/prodata/1/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/prodata/1/pubpna/US09\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/prodata/1/pubpna/US10\_PUBCOMB.seq.\*
- 14: /cgn2\_6/prodata/1/pubpna/US10B\_PUBCOMB.seq.\*
- 15: /cgn2\_6/prodata/1/pubpna/US10C\_PUBCOMB.seq.\*
- 16: /cgn2\_6/prodata/1/pubpna/US10D\_PUBCOMB.seq.\*
- 17: /cgn2\_6/prodata/1/pubpna/US10E\_PUBCOMB.seq.\*
- 18: /cgn2\_6/prodata/1/pubpna/US11\_NEW\_PUB.seq.\*
- 19: /cgn2\_6/prodata/1/pubpna/US11\_NEW\_PUB.seq.\*
- 20: /cgn2\_6/prodata/1/pubpna/US60\_NEW\_PUB.seq.\*
- 21: /cgn2\_6/prodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	142	100.0	429	17 US-10-665-975-1	Sequence 1, Appl
2	142	100.0	1619	9 US-09-918-186A-97	Sequence 97, Appl
3	142	100.0	1619	15 US-10-181-316-97	Sequence 97, Appl
4	142	100.0	1619	15 US-10-172-118-566	Sequence 566, Appl
5	142	100.0	1619	15 US-10-388-360-324	Sequence 324, Appl
6	142	100.0	1619	16 US-10-342-887-566	Sequence 566, Appl
7	142	100.0	1619	17 US-10-283-975A-445	Sequence 445, Appl
8	142	100.0	1619	17 US-10-657-022-99	Sequence 99, Appl
9	142	100.0	1643	18 US-10-807-897-1	Sequence 1, Appl
10	142	100.0	2404	13 US-10-071-766-109	Sequence 109, Appl
11	142	100.0	2404	15 US-10-084-817-285	Sequence 285, Appl
12	128	90.1	2570	17 US-10-741-601-210	Sequence 210, Appl
13	128	90.1	2585	17 US-10-741-601-216	Sequence 216, Appl
14	113	79.6	578	17 US-10-741-601-213	Sequence 213, Appl
15	93	65.5	740	16 US-10-305-720-918	Sequence 918, Appl
16	74	52.1	2639	17 US-10-741-601-215	Sequence 215, Appl
17	74	52.1	2654	17 US-10-741-601-211	Sequence 211, Appl
18	73	51.4	2452	17 US-10-741-601-212	Sequence 212, Appl
19	73	51.4	2467	17 US-10-741-601-214	Sequence 214, Appl
20	41	28.9	955	9 US-09-918-186A-10	Sequence 10, Appl
21	41	28.9	955	15 US-10-181-316-10	Sequence 10, Appl
22	41	28.9	955	18 US-10-807-897-3	Sequence 3, Appl
23	40	28.2	121	15 US-10-179-730-33	Sequence 33, Appl
24	39	27.5	14795	15 US-10-181-316-3	Sequence 3, Appl
25	39	27.5	14796	9 US-09-954-456-973	Sequence 973, Appl
26	39	27.5	14796	9 US-09-954-456-1636	Sequence 1636, Appl
27	39	27.5	14796	9 US-09-918-186A-3	Sequence 3, Appl
28	39	27.5	14796	9 US-09-880-107-3421	Sequence 3421, Appl
29	39	27.5	14796	11 US-09-968-007A-522	Sequence 522, Appl
30	39	27.5	14796	15 US-10-138-618-35	Sequence 35, Appl
31	39	27.5	23393	17 US-10-741-601-5680	Sequence 5680, Appl
32	39	27.5	41399	15 US-10-741-601-5768	Sequence 5768, Appl
33	36	25.4	120	15 US-10-029-386-23672	Sequence 23672, A
34	36	25.4	555	15 US-10-029-386-9972	Sequence 9972, Ap
35	36	25.4	1100	14 US-10-108-877-2	Sequence 2, Appl
36	33	23.2	201	17 US-10-741-601-4404	Sequence 4404, Ap
37	33	23.2	201	17 US-10-741-601-4415	Sequence 4415, Ap
38	33	23.2	201	17 US-10-741-601-4451	Sequence 4451, Ap
39	33	23.2	201	17 US-10-741-601-4462	Sequence 4462, Ap
40	29	20.4	13575	17 US-10-741-601-4463	Sequence 4463, Ap
41	23	16.2	144	17 US-10-741-601-4411	Sequence 4411, Ap
42	23	16.2	144	17 US-10-741-601-4423	Sequence 4423, Ap
43	23	16.2	144	17 US-10-741-601-4434	Sequence 4434, Ap
44	23	16.2	144	17 US-10-741-601-4436	Sequence 4436, Ap
45	23	16.2	144	17 US-10-741-601-4447	Sequence 4447, Ap

## ALIGNMENTS

RESULT 1  
US-10-665-975-1  
; Sequence 1, Application US/10665975  
; Publication No. US20040138119A1  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John C.  
; APPLICANT: Tamm, Ingo  
; TITLE OF INVENTION: USE OF HEPATITIS VIRUS B X-INTERACTING  
; FILE REFERENCE: BURHAM,005A  
; CURRENT APPLICATION NUMBER: US/10/665,975  
; PRIOR FILING DATE: 2003-09-18  
; PRIOR APPLICATION NUMBER: 60/412,109  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 429  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-665-975-1

## Alignment Scores:

Pred. No.: 5,61e-145 Length: 429  
 Score: 142.00 Matches: 142  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 17 Gaps: 0

US-09-690-825-34 (1-142) x US-10-665-975-1 (1-429)

QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20  
 Db 1 ATGGGTGCCCCGAGCTTGCCCCCTGCTGAGCCCTTTCTCAAGAGCAACCGCATCTCT 60  
 QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40  
 Db 61 ACATTCAAGAACTGGCCCTTCTTGAGAGGCTGGCCCTGACCCCGAGCGGATGGCCGAG 120  
 QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspPheLysIleGlnCysPhePheCys 60  
 Db 121 GCTGGCTTCATCCACTGCCCCCACTGAGAGAGAGCCCACTTGCCCTGATGTTCTTCTTGC 180  
 QY 61 PheLysGluLeuGluGlyTrpGluProAspAspAspProIleGluGluHisLysLysHis 80  
 Db 181 TTCAAGAGAGCTGGAAGGCTGGAGCCAGATGACGACCCCATAGAGAACTATAAAGCAT 240  
 QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100  
 Db 241 TCGTCGGGTTCGCTTTCCTTCTGTCAGAGAGAGTTGAAAGATTAACTTGGTGA 300  
 QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120  
 Db 301 TTTTGAACCTGCAGCAAGAAAGAGCCAGCAAAATTGCAGAGAAACCAACCAATAG 360  
 QY 121 LysLysGluPheGluGluThrAlaLysValArgArgAlaIleGluGlnLeuAlaAla 140  
 Db 361 AAGAAAGAAATTGTGAGAACTGCGAAGAAAGTGGCCGCTGCATCGAGCTGGCTGCC 420  
 QY 141 MetAsp 142  
 Db 421 ATGGAT 426

## RESULT 2

US-09-918-186A-97  
 ; Sequence 97, Application US/09918186A  
 ; Patent No. US20020137708A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: C. Frank Bennett  
 ; APPLICANT: Elizabeth J. Ackermann  
 ; APPLICANT: Eric E. Swayze  
 ; APPLICANT: Lex M. Cowsett  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION  
 ; FILE REFERENCE: ISPH-0585  
 ; CURRENT APPLICATION NUMBER: US/09/918,186A  
 ; PRIOR FILING DATE: 2001-07-30  
 ; PRIOR APPLICATION NUMBER: 09/496,694  
 ; PRIOR FILING DATE: 2000-02-02  
 ; PRIOR APPLICATION NUMBER: 09/286,407  
 ; PRIOR FILING DATE: 1999-04-05  
 ; PRIOR APPLICATION NUMBER: 09/163,162  
 ; PRIOR FILING DATE: 1998-09-29  
 ; NUMBER OF SEQ ID NOS: 250  
 ; SEQ ID NO 97  
 ; LENGTH: 1619  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-918-186A-97

Alignment Scores:  
 Pred. No.: 1.89e-144 Length: 1619  
 Score: 142.00 Matches: 142  
 Percent Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: Gaps: 0

Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0

US-09-690-825-34 (1-142) x US-09-918-186A-97 (1-1619)

QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20  
 Db 50 ATGGGTGCCCCGAGCTTGCCCCCTGCTGAGCCCTTTCTCAAGAGCAACCGCATCTCT 109  
 QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40  
 Db 110 ACATTCAAGAACTGGCCCTTCTTGAGAGGCTGGCCCTGACCCCGAGCGGATGGCCGAG 169  
 QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspPheLysIleGlnCysPhePheCys 60  
 Db 170 GCTGGCTTCATCCACTGCCCCCACTGAGAGAGAGCCCACTTGCCCTGATGTTCTTCTTGC 229  
 QY 61 PheLysGluLeuGluGlyTrpGluProAspAspAspProIleGluGluHisLysLysHis 80  
 Db 230 TTCAAGAGAGCTGGAAGGCTGGAGCCAGATGACGACCCCATAGAGAACTATAAAGCAT 289  
 QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100  
 Db 290 TCGTCGGGTTCGCTTTCCTTCTGTCAGAGAGAGTTGAAAGATTAACTTGGTGA 349  
 QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120  
 Db 350 TTTTGAACCTGCAGCAAGAAAGAGCCAGCAAAATTGCAGAGAAACCAACCAATAG 409  
 QY 121 LysLysGluPheGluGluThrAlaLysValArgArgAlaIleGluGlnLeuAlaAla 140  
 Db 410 AAGAAAGAAATTGTGAGAACTGCGAAGAAAGTGGCCGCTGCATCGAGCTGGCTGCC 469  
 QY 141 MetAsp 142  
 Db 470 ATGGAT 475

## RESULT 3

US-10-181-316-97  
 ; Sequence 97, Application US/10181316  
 ; Publication No. US20030211607A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: C. Frank Bennett  
 ; APPLICANT: Elizabeth J. Ackermann  
 ; APPLICANT: Eric E. Swayze  
 ; APPLICANT: Lex M. Cowsett  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION  
 ; FILE REFERENCE: ISPH-0650  
 ; CURRENT APPLICATION NUMBER: US/10/181,316  
 ; PRIOR FILING DATE: 2002-07-16  
 ; PRIOR APPLICATION NUMBER: PCT/US01/02939  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: 09/496,694  
 ; PRIOR FILING DATE: 2000-02-02  
 ; PRIOR APPLICATION NUMBER: 09/286,407  
 ; PRIOR FILING DATE: 1999-04-05  
 ; PRIOR APPLICATION NUMBER: 09/163,162  
 ; PRIOR FILING DATE: 1998-09-29  
 ; NUMBER OF SEQ ID NOS: 249  
 ; SEQ ID NO 97  
 ; LENGTH: 1619  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-10-181-316-97

Alignment Scores:  
 Pred. No.: 1.89e-144 Length: 1619  
 Score: 142.00 Matches: 142  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 15 Gaps: 0

US-09-690-825-34 (1-142) x US-10-181-316-97 (1-1619)

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QY 1 MetGlyAlaProThrLeuProProAlaATrpgInProPheLeuLysAspHisArgIleSer 20
Db 50 ATGGGTGCCCCGACGTTGCCCCCTGCTGCGACGCCCTTTCTCAAGACCAACCGCATCTCT 109
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db 110 ACATTCAAGAACTGGCCCTTCTTGAGGGGTGGCCCTGACCCCGAGCGGATGGCCGAG 169
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
Db 170 GCTGCTTCATCCACTGCCCCCTGAGAACGAGCCGACTGGCCCGCAGTGTCTTCTGTC 229
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis 80
Db 230 TTCAAGAGCTGGAAGGCTGGAGCCAGATGACGACCCCTTAGAGAACTTAAATAAACAT 289
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
Db 290 TCGTCCGGTTCGCTTCTTCTTCTGTCAGAACAGCTTGAAGATTAACTTGGTGA 349
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
Db 350 TTTTGAACCTGACACAGAAAGCCAGAACAAATTGCAAGGAAACCAACATAAG 409
QY 121 LysLysGluPheGluGluThrAlaLysValArgArgAlaIleGluGlnLeuAlaAla 140
Db 410 AAGAAAGAAATTGAGGAACCTGCAAGAAAGTCCGCGTCCATCGACGACCTGGCTGCC 469
QY 141 MetAsp 142
Db 470 ATGGAT 475
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## RESULT 4

```
US-10-172-118-566
; Sequence 566, Application US/10172118
; Publication No. US2003024374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, HongYue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 566
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-566
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## Alignment Scores:

```
Pred. No.: 1,89e-144 Length: 1619
Score: 142.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0
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US-09-690-825-34 (1-142) x US-10-172-118-566 (1-1619)

```
QY 1 MetGlyAlaProThrLeuProProAlaATrpgInProPheLeuLysAspHisArgIleSer 20
Db 50 ATGGGTGCCCCGACGTTGCCCCCTGCTGCGACGCCCTTTCTCAAGACCAACCGCATCTCT 109
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db 110 ACATTCAAGAACTGGCCCTTCTTGAGGGGTGGCCCTGACCCCGAGCGGATGGCCGAG 169
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
Db 170 GCTGCTTCATCCACTGCCCCCTGAGAACGAGCCGACTGGCCCGCAGTGTCTTCTGTC 229
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis 80
Db 230 TTCAAGAGCTGGAAGGCTGGAGCCAGATGACGACCCCTTAGAGAACTTAAATAAACAT 289
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
Db 290 TCGTCCGGTTCGCTTCTTCTTCTGTCAGAACAGCTTGAAGATTAACTTGGTGA 349
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
Db 350 TTTTGAACCTGACACAGAAAGCCAGAACAAATTGCAAGGAAACCAACATAAG 409
QY 121 LysLysGluPheGluGluThrAlaLysValArgArgAlaIleGluGlnLeuAlaAla 140
Db 410 AAGAAAGAAATTGAGGAACCTGCAAGAAAGTCCGCGTCCATCGACGACCTGGCTGCC 469
QY 141 MetAsp 142
Db 470 ATGGAT 475
```

## RESULT 5

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US-10-388-360-324
; Sequence 324, Application US/10388360
; Publication No. US2003025528A1
; GENERAL INFORMATION:
; APPLICANT: GENOMIC HEALTH
; APPLICANT: Baker, Joffre B.
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Kiefer, Michael C.
; APPLICANT: Shak, Steve
; TITLE OF INVENTION: GENE EXPRESSION PROFILING IN BIOPSIED TUMOR TISSUES
; FILE REFERENCE: 39740-0001US
; CURRENT APPLICATION NUMBER: US/10/388,360
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/412,049
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US 60/364,890
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 324
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-388-360-324
```

## Alignment Scores:

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Pred. No.: 1,89e-144 Length: 1619
Score: 142.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0
```

US-09-690-825-34 (1-142) x US-10-388-360-324 (1-1619)

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QY 1 MetGlyAlaProThrLeuProProAlaATrpgInProPheLeuLysAspHisArgIleSer 20
Db 50 ATGGGTGCCCCGACGTTGCCCCCTGCTGCGACGCCCTTTCTCAAGACCAACCGCATCTCT 109
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QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40  
DB 110 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGCGCTGCACCCCGAGCGGATGGCCGAG 169  
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60  
DB 170 GCTGGCTTCACTGACCTGCCCACTGAGAACGACGACCTGGCCCGAGTGTCTTCTTGC 229  
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHis 80  
DB 230 TTCAGAGAGCTGGAAGCTGGAGCCAGATGACGCCCTTGAAGAACTTAAATAAAGCAT 289  
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100  
DB 290 TCGCCGGTTCGCTTCTTCTTCTGTCAGAGACAGTTGAAGATTAACTTGGTGA 349  
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120  
DB 350 TTTTGAACCTGGACAGAGAAAGGCCAGAACAAATTGCAAGGAAACCAACATTAAG 409  
QY 121 LysLysGluPheGluGluThrAlaLysValArgArgAlaIleGluGluLeuAla 140  
DB 410 AAGAAAGATTGAGAGAACTGCGAGAAAGTGGCCGCTGCATCGAGCGCTGGCC 469  
QY 141 MetAsp 142  
DB 470 ATGGAT 475

## RESULT 6

US-10-342-887-566  
Sequence 566, Application US/10342887  
Publication No. US20040058340A1  
GENERAL INFORMATION:  
APPLICANT: Dai, Hongyue  
APPLICANT: He, Yidong  
APPLICANT: Linsley, Peter S.  
APPLICANT: Mao, Mao  
APPLICANT: Roberts, Christopher J.  
APPLICANT: Van 't Veer, Laura Johanna  
APPLICANT: Van de Vijver, Marc J.  
APPLICANT: Bernards, Rene  
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients  
FILE REFERENCE: 9301-188-999  
CURRENT APPLICATION NUMBER: US/10/342,887  
CURRENT FILING DATE: 2003-01-15  
PRIOR APPLICATION NUMBER: 60/298,918  
PRIOR FILING DATE: 2001-06-18  
PRIOR APPLICATION NUMBER: 60/380,710  
PRIOR FILING DATE: 2002-05-14  
PRIOR APPLICATION NUMBER: 10/172,118  
PRIOR FILING DATE: 2002-06-14  
NUMBER OF SEQ ID NOS: 2699  
SEQ ID NO 566  
LENGTH: 1619  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-342-887-566

## Alignment Scores:

Pred. No.: 1,89e-144 Length: 1619  
Score: 142.00 Matches: 142  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 16 Gaps: 0

US-09-690-825-34 (1-142) x US-10-342-887-566 (1-1619)

QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20  
DB 50 ATGGGTGCGCCGACGTTGCGCCCTGCTGGACGCCCTTCTCAAGAGCAACCGCATCTCT 109

QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40  
DB 110 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGCGCTGCACCCCGAGCGGATGGCCGAG 169  
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60  
DB 170 GCTGGCTTCACTGACCTGCCCACTGAGAACGACGACCTGGCCCGAGTGTCTTCTTGC 229  
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHis 80  
DB 230 TTCAGAGAGCTGGAAGCTGGAGCCAGATGACGCCCTTGAAGAACTTAAATAAAGCAT 289  
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100  
DB 290 TCGCCGGTTCGCTTCTTCTTCTGTCAGAGACAGTTGAAGATTAACTTGGTGA 349  
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120  
DB 350 TTTTGAACCTGGACAGAGAAAGGCCAGAACAAATTGCAAGGAAACCAACATTAAG 409  
QY 121 LysLysGluPheGluGluThrAlaLysValArgArgAlaIleGluGluLeuAla 140  
DB 410 AAGAAAGATTGAGAGAACTGCGAGAAAGTGGCCGCTGCATCGAGCGCTGGCC 469  
QY 141 MetAsp 142  
DB 470 ATGGAT 475

## RESULT 7

US-10-283-975A-445  
Sequence 445, Application US/10283975A  
Publication No. US20040110792A1  
GENERAL INFORMATION:  
APPLICANT: Ortho-Clinical Diagnostics, Inc.  
TITLE OF INVENTION: Methods For Assessing and Treating Leukemia  
FILE REFERENCE: CDS 293 PCT  
CURRENT APPLICATION NUMBER: US/10/283,975A  
CURRENT FILING DATE: 2002-10-30  
PRIOR APPLICATION NUMBER: 60/340,938  
PRIOR FILING DATE: 2001-10-30  
PRIOR APPLICATION NUMBER: 60/338,997  
PRIOR FILING DATE: 2001-10-30  
PRIOR APPLICATION NUMBER: 60/340,081  
PRIOR FILING DATE: 2001-10-30  
PRIOR APPLICATION NUMBER: 60/341,012  
PRIOR FILING DATE: 2001-10-30  
SOFTWARE: PatentIn version 3.1  
NUMBER OF SEQ ID NOS: 900  
SEQ ID NO 445  
LENGTH: 1619  
TYPE: DNA  
ORGANISM: HUMAN  
US-10-283-975A-445

## Alignment Scores:

Pred. No.: 1,89e-144 Length: 1619  
Score: 142.00 Matches: 142  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 17 Gaps: 0

US-09-690-825-34 (1-142) x US-10-283-975A-445 (1-1619)

QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20  
DB 50 ATGGGTGCGCCGACGTTGCGCCCTGCTGGACGCCCTTCTCAAGAGCAACCGCATCTCT 109  
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40  
DB 110 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGCGCTGCACCCCGAGCGGATGGCCGAG 169  
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60

Db 170 GGTGGCTTCATCCACGCGCCCACTGGAACGAGCAGATCTTGCCAGGTTCTTCGCGC 229

Qy 61 PheLysGluLeuGlnGlyTTPGluProAspAspProIleGluGlnHisLysLysHis 80

Db 230 TTCAAGAGAGCTGGAGAGCTGGAGAGCAGATGACGAGCCCATGAGAGACATTAAGAGCAT 289

Qy 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100

Db 290 TCGTCCGGTTGGCTTCTTCCTTCTGTCAGAGAGCAGTTGAAGAAATTAACCTTGCTGAA 349

Qy 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120

Db 350 TTTTGAAGACTGGACAGAGAAAGCCAAAGCAAAATTGCAAGAGAAACCAACATTAAG 409

Qy 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAlaAla 140

Db 410 AAGAAGAAATTTGAGAAAGCTGGAGAAAGTGGCCGTCATGAGCAGCTGGCTGCC 469

Qy 141 MetAsp 142

Db 470 ATGGAT 475

RESULT 8

US-10-657-022-99

Sequence 99, Application US/10657022

Publication No. US20040180354A1

GENERAL INFORMATION:

APPLICANT: Simard, John J. L.

APPLICANT: Diamond, David C.

APPLICANT: Liu, Liping

TITLE OF INVENTION: EPTROPE SEQUENCES

FILE REFERENCE: MANKK.032A

CURRENT FILING DATE: 2003-09-04

PRIOR APPLICATION NUMBER: 60/409123

PRIOR FILING DATE: 2002-09-06

NUMBER OF SEQ ID NOS: 610

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 99

LENGTH: 1619

TYPE: DNA

ORGANISM: Homo sapiens

US-10-657-022-99

Alignment Scores:

Pred. No.: 1,89e-144 Length: 1619

Score: 142.00 Matches: 142

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 17 Gaps: 0

US-09-690-825-34 (1-142) x US-10-657-022-99 (1-1619)

Qy 1 MetGlyAlaProThrLeuProProAlaTTPGlnProPheLeuLysAspHisArgIleSer 20

Db 50 ATGGAGTCCCGGACGCTGGCCCTGCTGCGACCCCTTCTCAAGAGACACCGCATCTCT 109

Qy 21 ThrPheLysAsnTTPProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40

Db 110 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGGCTGCAACCCGAGCGGATGCGCGAG 169

Qy 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60

Db 170 GCTGGCTTCATCCACTGCCCCCACTGAGAGAGAGCCAGACTTGCCCAAGTCTTCTCTGC 229

Qy 61 PheLysGluLeuGluGlyTTPGluProAspAspAspProIleGluGlnHisLysLysHis 80

Db 230 TTCAAGAGAGCTGGAGAGCTGGAGAGCAGATGACGAGCCCATTAAGAGAACTTAAGAGCAT 289

Qy 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100

Db 290 TCGTCCGGTTGGCTTCTTCCTTCTGTCAGAGAGCAGTTGAAGAAATTAACCTTGCTGAA 349

Qy 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120

Db 350 TTTTGAAGACTGGACAGAGAAAGCCAAAGCAAAATTGCAAGAGAAACCAACATTAAG 409

Qy 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAlaAla 140

Db 410 AAGAAGAAATTTGAGAAAGCTGGAGAAAGTGGCCGTCATGAGCAGCTGGCTGCC 469

Qy 141 MetAsp 142

Db 470 ATGGAT 475

RESULT 9

US-10-807-897-1

Sequence 1, Application US/10807897

Publication No. US20040192631A1

GENERAL INFORMATION:

APPLICANT: Xiang, Rong

APPLICANT: Zhou, He

APPLICANT: Reisfeld, Ralph A.

TITLE OF INVENTION: DNA VACCINES AGAINST TUMOR GROWTH AND

TITLE OF INVENTION: METHODS OF USE THEREOF

FILE REFERENCE: TSRI-874.1

CURRENT FILING DATE: 2004-03-24

PRIOR APPLICATION NUMBER: 60/457,009

PRIOR FILING DATE: 2003-03-24

NUMBER OF SEQ ID NOS: 29

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1

LENGTH: 1643

TYPE: DNA

ORGANISM: HOMO SAPIENS

US-10-807-897-1

Alignment Scores:

Pred. No.: 1,92e-144 Length: 1643

Score: 142.00 Matches: 142

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 18 Gaps: 0

US-09-690-825-34 (1-142) x US-10-807-897-1 (1-1643)

Qy 1 MetGlyAlaProThrLeuProProAlaTTPGlnProPheLeuLysAspHisArgIleSer 20

Db 45 ATGGAGTCCCGGACGCTGGCCCTGCTGCGACCCCTTCTCAAGAGACACCGCATCTCT 104

Qy 21 ThrPheLysAsnTTPProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40

Db 105 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGGCTGCAACCCGAGCGGATGCGCGAG 164

Qy 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60

Db 165 GCTGGCTTCATCCACTGCCCCCACTGAGAGAGAGCCAGACTTGCCCAAGTCTTCTCTGC 224

Qy 61 PheLysGluLeuGluGlyTTPGluProAspAspAspProIleGluGlnHisLysLysHis 80

Db 225 TTCAAGAGAGCTGGAGAGCTGGAGAGCAGATGACGAGCCCATTAAGAGAACTTAAGAGCAT 284

Qy 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100

Db 285 TCGTCCGGTTGGCTTCTTCCTTCTGTCAGAGAGCAGTTGAAGAAATTAACCTTGCTGAA 344

Qy 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120

Db 345 TTTTGAAGACTGGACAGAGAAAGCCAAAGCAAAATTGCAAGAGAAACCAACATTAAG 404

QY 121 LysylsglupehgiugluthrAlaValArgAlaIleleugluInleuAla140  
DB 405 AAGAAAGAAATTTGGAGAACTGGCAAGAAAGTGGCGCTGCATCGAGCGCTGGCTGCC 464  
QY 141 Metasp 142  
DB 465 ATGGAT 470

RESULT 10  
US-10-071-766-109  
; Sequence 109, Application US/10071766  
; Publication No. US20020192678A1  
; GENERAL INFORMATION:  
; APPLICANT: Huel-Mei Chen  
; TITLE OF INVENTION: GENES EXPRESSED IN SENESENCE  
; FILE REFERENCE: PA-0043 US  
; CURRENT APPLICATION NUMBER: US/10/071,766  
; PRIOR FILING DATE: 2002-02-07  
; NUMBER OF SEQ ID NOS: 144  
; SOFTWARE: PERL Program  
; SEQ ID NO 109  
; LENGTH: 2404  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; OTHER INFORMATION: Incyte ID No. US20020192678A1 251651.4  
; NAME/KEY: unsure  
; LOCATION: 710, 717, 724, 982-1007  
; OTHER INFORMATION: a, t, c, g, or other  
US-10-071-766-109

Alignment Scores:  
Pred. No.: 2,71e-144 Length: 2404  
Score: 142.00 Matches: 142  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 13 Gaps: 0

US-09-690-825-34 (1-142) x US-10-071-766-109 (1-2404)

QY 1 MetGlyAlaProThrIleuProProAlaITrpgInProPheLeuLysAspHisArgIleSer 20  
DB 56 ATGGGTGCCCCGAGGTGGCCCCCTGGCTGGAGCCCTTTCTCAAGAGCCACCGCATCTCT 115  
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40  
DB 116 ACATTCAAGAACTGGCCCTTCTTGAAGGCTGGCGCTGCACCCCGAGCGGATGGCCGAG 175  
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60  
DB 176 GCTGGCTTCACTCCACTGCCCACTGAGAACGAGCCAGACTGGCCAGTGTTCCTCTGC 235  
QY 61 PheLysGluLeuGluGlyITrpgIuProAspAspProIleGluIuHisLysLysHis 80  
DB 236 TTCAAGAGAGCTGGAAGCTGGAGCCAGATGACGCCCATTAAGAACTAAAGCAT 295  
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100  
DB 296 TCGTCCGCTTGGCTTCTTCTTCTGTCAGAGAGAGTTTAAAGATTAAACCTTGTGTGA 355  
QY 101 PheLeuLysLeuAspArgIuArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120  
DB 356 TTTTGAACCTGGAAGAGAAAGCCAAACAAATTTCAGAAAGAAACCAACATAAG 415  
QY 121 LysLysGluPheGluGluIuThrAlaLysValArgArgAlaIleleugluInleuAla140  
DB 416 AAGAAAGAAATTTGGAGAACTGGCAAGAAAGTGGCGCTGCATCGAGCGCTGGCTGCC 475  
QY 141 Metasp 142  
DB 476 ATGGAT 481

RESULT 11  
US-10-084-817-285  
; Sequence 285, Application US/10084817  
; Publication No. US20030119009A1  
; GENERAL INFORMATION:  
; APPLICANT: Susan Stuart  
; APPLICANT: Jed G. Nuchtern  
; APPLICANT: Sharon E. Plon  
; APPLICANT: Jason M. Shohet  
; TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION  
; FILE REFERENCE: PA-0046 US  
; CURRENT APPLICATION NUMBER: US/10/084,817  
; PRIOR FILING DATE: 2002-02-25  
; PRIOR APPLICATION NUMBER: 60/270,784  
; PRIOR FILING DATE: 2001-02-23  
; NUMBER OF SEQ ID NOS: 365  
; SOFTWARE: PERL Program  
; SEQ ID NO 285  
; LENGTH: 2404  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; OTHER INFORMATION: Incyte ID No. US20030119009A1 251651.4  
; NAME/KEY: unsure  
; LOCATION: 710, 717, 724  
; OTHER INFORMATION: a, t, c, g, or other  
US-10-084-817-285

Alignment Scores:  
Pred. No.: 2,71e-144 Length: 2404  
Score: 142.00 Matches: 142  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 15 Gaps: 0

US-09-690-825-34 (1-142) x US-10-084-817-285 (1-2404)

QY 1 MetGlyAlaProThrIleuProProAlaITrpgInProPheLeuLysAspHisArgIleSer 20  
DB 56 ATGGGTGCCCCGAGGTGGCCCCCTGGCTGGAGCCCTTTCTCAAGAGCCACCGCATCTCT 115  
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40  
DB 116 ACATTCAAGAACTGGCCCTTCTTGAAGGCTGGCGCTGCACCCCGAGCGGATGGCCGAG 175  
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60  
DB 176 GCTGGCTTCACTCCACTGCCCACTGAGAACGAGCCAGACTGGCCAGTGTTCCTCTGC 235  
QY 61 PheLysGluLeuGluGlyITrpgIuProAspAspProIleGluIuHisLysLysHis 80  
DB 236 TTCAAGAGAGCTGGAAGCTGGAGCCAGATGACGCCCATTAAGAACTAAAGCAT 295  
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100  
DB 296 TCGTCCGCTTGGCTTCTTCTTCTGTCAGAGAGAGTTTAAAGATTAAACCTTGTGTGA 355  
QY 101 PheLeuLysLeuAspArgIuArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120  
DB 356 TTTTGAACCTGGAAGAGAAAGCCAAACAAATTTCAGAAAGAAACCAACATAAG 415  
QY 121 LysLysGluPheGluGluIuThrAlaLysValArgArgAlaIleleugluInleuAla140  
DB 416 AAGAAAGAAATTTGGAGAACTGGCAAGAAAGTGGCGCTGCATCGAGCGCTGGCTGCC 475  
QY 141 Metasp 142  
DB 476 ATGGAT 481

RESULT 12



```
US-10-741-601-210
; Sequence 210, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL0001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 210
; LENGTH: 2570
; TYPE: DNA
; ORGANISM: Homo sapiens
;
Alignment Scores:
Pred. No.: 4,83e-129 Length: 2570
Score: 128.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 90.14% Indels: 0
DB: 17 Gaps: 0
US-09-690-825-34 (1-142) x US-10-741-601-210 (1-2570)
QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
DB 75 ATGGGTGCCCGACGCTGGCCCTGCTGCGACGCCCTTCTCAAGACCAACCGCATCTCT 134
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 135 ACATTCAAGAACTGGCCCTTCTTGAGAGGCTGCGCTGCACCCCGAGCGGATGGCCGAG 194
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspPheIleGluHisLysLysHis 60
DB 195 GCTGCTTCATCCACTGCGCCCACTGAGAACGAGCCAGACTGGCCCAAGTTCTCTCTGC 254
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluHisLysLysHis 80
DB 255 TTCAAGAGCTGGAAGGCTGGAGCCAGATGACGACCCCATTAAGAAATTAATAAGCAT 314
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
DB 315 TCGTCCGCTGCGCTTCTCTTCTGTCAGAAACAGATTGAAGATTAAACCTGGTGAA 374
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
DB 375 TTTTGAAGCTGACAGAGAAAGACCAACAAATTGCAAGAAACCAACCAATAG 434
QY 121 LysLysGluPheGluGluThrAla 128
DB 435 AAGAAAGAAATTTGAGGAAACTGCG 458
;
RESULT 13
US-10-741-601-216
; Sequence 216, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL0001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 216
; LENGTH: 2585
; TYPE: DNA
; ORGANISM: Homo sapiens
;
Alignment Scores:
Pred. No.: 4,86e-129 Length: 2585
Score: 128.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 90.14% Indels: 0
DB: 17 Gaps: 0
US-09-690-825-34 (1-142) x US-10-741-601-216 (1-2585)
QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
DB 75 ATGGGTGCCCGACGCTGGCCCTGCTGCGACGCCCTTCTCAAGACCAACCGCATCTCT 134
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 135 ACATTCAAGAACTGGCCCTTCTTGAGAGGCTGCGCTGCACCCCGAGCGGATGGCCGAG 194
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspPheIleGluHisLysLysHis 60
DB 195 GCTGCTTCATCCACTGCGCCCACTGAGAACGAGCACTGGCCCAAGTTCTCTCTGCG 254
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluHisLysLysHis 80
DB 255 TTCAAGAGCTGGAAGGCTGGAGCCAGATGACGACCCCATTAAGAAATTAATAAGCAT 314
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
DB 315 TCGTCCGCTGCGCTTCTCTTCTGTCAGAAAGAGATTGAAGATTAAACCTGGTGAA 374
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
DB 375 TTTTGAAGCTGACAGAGAAAGACCAAGCAACAAATTGCAAGAAACCAACCAATAG 434
QY 121 LysLysGluPheGluGluThrAla 128
DB 435 AAGAAAGAAATTTGAGGAAACTGCG 458
;
RESULT 14
US-10-741-601-213
; Sequence 213, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL0001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 213
; LENGTH: 578
; TYPE: DNA
; ORGANISM: Homo sapiens
;
Alignment Scores:
Pred. No.: 2,53e-113 Length: 578
Score: 113.00 Matches: 113
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 79.58% Indels: 0
DB: 17 Gaps: 0
US-09-690-825-34 (1-142) x US-10-741-601-213 (1-578)
QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
DB 75 ATGGGTGCCCGACGCTGGCCCTGCTGCGACGCCCTTCTCAAGACCAACCGCATCTCT 134
```

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US-10-741-601-216
; Sequence 210, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL0001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 210
; LENGTH: 2570
; TYPE: DNA
; ORGANISM: Homo sapiens
;
Alignment Scores:
Pred. No.: 4,86e-129 Length: 2585
Score: 128.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 90.14% Indels: 0
DB: 17 Gaps: 0
US-09-690-825-34 (1-142) x US-10-741-601-216 (1-2585)
QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
DB 75 ATGGGTGCCCGACGCTGGCCCTGCTGCGACGCCCTTCTCAAGACCAACCGCATCTCT 134
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
DB 135 ACATTCAAGAACTGGCCCTTCTTGAGAGGCTGCGCTGCACCCCGAGCGGATGGCCGAG 194
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspPheIleGluHisLysLysHis 60
DB 195 GCTGCTTCATCCACTGCGCCCACTGAGAACGAGCACTGGCCCAAGTTCTCTCTGCG 254
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluHisLysLysHis 80
DB 255 TTCAAGAGCTGGAAGGCTGGAGCCAGATGACGACCCCATTAAGAAATTAATAAGCAT 314
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
DB 315 TCGTCCGCTGCGCTTCTCTTCTGTCAGAAAGAGATTGAAGATTAAACCTGGTGAA 374
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
DB 375 TTTTGAAGCTGACAGAGAAAGACCAAGCAACAAATTGCAAGAAACCAACCAATAG 434
QY 121 LysLysGluPheGluGluThrAla 128
DB 435 AAGAAAGAAATTTGAGGAAACTGCG 458
;
RESULT 14
US-10-741-601-213
; Sequence 213, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL0001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 213
; LENGTH: 578
; TYPE: DNA
; ORGANISM: Homo sapiens
;
Alignment Scores:
Pred. No.: 2,53e-113 Length: 578
Score: 113.00 Matches: 113
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 79.58% Indels: 0
DB: 17 Gaps: 0
US-09-690-825-34 (1-142) x US-10-741-601-213 (1-578)
QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20
DB 75 ATGGGTGCCCGACGCTGGCCCTGCTGCGACGCCCTTCTCAAGACCAACCGCATCTCT 134
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QY 21 ThrPheLysAsnTTPProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40  
Db 135 ACATTCAAGAACTGGCCCTTCTTGGAGGCTGGCCCTGCACCCCGAGCGATGGCCGAG 194  
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60  
Db 195 GCTGGCTTCATCCCTCCCTCCCTGAGAGACGAGCGACACTGGCCCGAGTCTTCTCTG 254  
QY 61 PheLysGluLeuGluGlyTTPGluProAspAspProIleGluGluHisLysLysHis 80  
Db 255 TTCAAGAGAGCTGGAGGCTGGAGCCGACATGACGCCCATAGAGAACTATAAAGCAT 314  
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGluGlu 100  
Db 315 TCGTCCGCTGGCTTCTTCTTCTTCTGTCAGAGAGAGCTTAAAGAAATTAACTTGGTGA 374  
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIle 113  
Db 375 TTTTGAAGCTGACAGAGAAAGAGCCAGAACAAAT 413

## RESULT 15

US-10-305-720-918  
/ Sequence 918, Application US/10305720  
/ Publication No. US20040010136A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.  
/ TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression  
/ FILE REFERENCE: PA-0002-CON  
/ CURRENT APPLICATION NUMBER: US/10/305,720  
/ PRIOR FILING DATE: 2002-11-26  
/ PRIORITY APPLICATION NUMBER: 09/016,434  
/ NUMBER OF SEQ ID NOS: 1490  
/ SOFTWARE: PERL Program  
/ SEQ ID NO 918  
/ LENGTH: 740  
/ TYPE: DNA  
/ ORGANISM: Homo sapiens  
/ FEATURE:  
/ NAME/KEY: misc feature  
/ OTHER INFORMATION: Incyte ID No. US20040010136A1 752848  
/ NAME/KEY: unsure  
/ LOCATION: (1) ... (740)  
/ OTHER INFORMATION: a, t, c, g, or other  
US-10-305-720-918

## Alignment Scores:

Pred. No.: 1,78e-91 Length: 740  
Score: 93.00 Matches: 130  
Percent Similarity: 98.48% Conservative: 0  
Best Local Similarity: 98.48% Mismatches: 1  
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DB: 16 Gaps: 0

US-09-690-825-34 (1-142) x US-10-305-720-918 (1-740)

QY 12 ProPheLeuLysAspHisArgIleSerThrPheLysAsnTTPProPheLeuGluGlyCys 31  
Db 51 CCCCTTCTCAAGAGCACCCGACATCTACATCAAGAACTGGCCCTTCTTGGAGGCTGC 110  
QY 32 AlaGlyThrProGluArgMetAlaGluAlaGlyPheIleHisCysProThrGlu-AsnGlu 51  
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QY 51 uProAspLeuAlaGlnCysPhePheCysPheLysGluLeuGluGlyTTPGluProAspAs 71  
Db 170 GCCAGACTTGGCCCGAGCTTCTCTCTGCTTCAAGAGACTGGAAGCTGGAGCCAGATGA 229  
QY 71 pAspProIleGluGluHisLysLysHisSerSerGlyCysAlaPheLeuSerValLysLys 91  
Db 230 CGACCCCATAGAGAGACATATAAAGCACTGCTCGGCTTCTTCTTCTGTCAGAA 289

QY 91 sGlnPheGluGluLeuThrLeuGluGluPheLeuLysLeuAspArgGluArgAlaLysAs 111  
Db 290 GCAGTTTGAAGAAATTAACCTTGTGAAATTTTGAACCTGACACAGAGAAAGCCAAAGAA 349  
QY 111 nLysIleAlaLysGluThrAsnAsnLysLysLysGluPheGluGluThrAlaLysLysVa 131  
Db 350 CAAATTTCCAAAGAGAAACCAATTAAGAAAGAAATTTGAGGAAACTGGAGAAAGT 409  
QY 131 lArgArgAlaIleGluGluLeuAlaAlaMetAsp 142  
Db 410 GCGCGTGCATCGAGCGAGCTGGCTGCCATGAT 443

Search completed: November 1, 2004, 21:47:03  
cod time : 373 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus.p2n model

Run on: November 1, 2004, 19:17:01 ; Search time 89 Seconds  
(without alignments)

1134.068 Million cell updates/sec

Title: US-09-690-825-34

Perfect score: 142  
Sequence: 1 MGAPFLPMAQOPFLXDRHS.....EFETAKVRAIEQLAAMD 142

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Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 824507 seqs, 355394441 residues

Word size: 1

Total number of hits satisfying chosen parameters: 1643611

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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Database:

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5: /cgn2\_6/prodata/1/ina/PCTUS\_COMB.seq.\*  
6: /cgn2\_6/prodata/1/ina/backfillseq1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysts of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	142	100.0	426	US-09-283-144-2	Sequence 2, Appl1
2	142	100.0	426	US-09-163-162-1	Sequence 1, Appl1
3	142	100.0	426	US-09-286-407-1	Sequence 1, Appl1
4	142	100.0	426	US-09-496-694B-97	Sequence 97, Appl1
5	107	75.4	1165	US-08-448-722A-1	Sequence 1, Appl1
6	107	75.4	1165	US-08-189-305B-1	Sequence 1, Appl1
7	93	65.5	740	US-09-016-434-918	Sequence 918, Appl1
8	76	53.5	399	US-09-513-999C-2315	Sequence 2315, Appl1
9	41	28.9	955	US-09-496-694B-10	Sequence 10, Appl1
10	39	27.5	14796	US-08-975-080-35	Sequence 35, Appl1
11	39	27.5	14796	US-09-630-706-10	Sequence 10, Appl1
12	39	27.5	14796	US-09-496-694B-3	Sequence 3, Appl1

13	37	26.1	417	3	US-09-283-144-1	Sequence 1, Appl1
14	9	6.3	30	4	US-09-672-717-199	Sequence 199, Appl1
15	8	5.6	26	3	US-09-496-694B-13	Sequence 13, Appl1
16	8	5.6	293	4	US-09-621-976-13359	Sequence 13359, A
17	8	5.6	326	4	US-09-621-976-13398	Sequence 13398, A
18	8	5.6	337	4	US-09-621-976-13367	Sequence 13367, A
19	8	5.6	342	4	US-09-621-976-13367	Sequence 13367, A
20	8	5.6	346	4	US-09-621-976-13443	Sequence 13443, A
21	8	5.6	349	4	US-09-621-976-13375	Sequence 13375, A
22	8	5.6	351	4	US-09-621-976-13407	Sequence 13407, A
23	8	5.6	357	4	US-09-621-976-13407	Sequence 13407, A
24	8	5.6	361	4	US-09-621-976-13392	Sequence 13392, A
25	8	5.6	365	4	US-09-621-976-13428	Sequence 13428, A
26	8	5.6	515	3	US-09-496-694B-231	Sequence 231, Appl1
27	8	5.6	707	4	US-09-270-767-11365	Sequence 11365, A
28	8	5.6	812	4	US-09-270-767-15067	Sequence 15067, A
29	8	5.6	4376	1	US-08-119-125A-2	Sequence 1, Appl1
30	8	5.6	6744	1	US-08-119-125A-2	Sequence 1, Appl1
31	7	4.9	21	3	US-09-163-162-2	Sequence 2, Appl1
32	7	4.9	21	3	US-09-286-407-2	Sequence 2, Appl1
33	7	4.9	21	3	US-09-496-694B-4	Sequence 4, Appl1
34	7	4.9	22	3	US-09-163-162-3	Sequence 3, Appl1
35	7	4.9	22	3	US-09-286-407-3	Sequence 3, Appl1
36	7	4.9	22	3	US-09-496-694B-5	Sequence 5, Appl1
37	7	4.9	23	3	US-09-163-162-4	Sequence 4, Appl1
38	7	4.9	23	3	US-09-286-407-4	Sequence 4, Appl1
39	7	4.9	23	3	US-09-496-694B-6	Sequence 6, Appl1
40	7	4.9	29	4	US-10-270-313-2	Sequence 2, Appl1
41	7	4.9	222	4	US-09-513-999C-29674	Sequence 29674, A
42	7	4.9	273	4	US-09-313-294A-1818	Sequence 1818, Appl1
43	7	4.9	310	3	US-09-328-111-715	Sequence 715, Appl1
44	7	4.9	504	4	US-09-107-532A-1678	Sequence 1678, Appl1
45	7	4.9	559	4	US-09-621-976-10449	Sequence 10449, A

#### ALIGNMENTS

RESULT 1  
US-09-283-144-2  
; Sequence 2, Application US/09283144  
; Patent No. 6346389  
; GENERAL INFORMATION:  
; APPLICANT: Yale University  
; TITLE OF INVENTION: Method for Selectively Modulating the Interactions  
; FILE REFERENCE: 44574-5033-US  
; CURRENT FILING DATE: 1999-04-01  
; EARLIER APPLICATION NUMBER: US 60/080, 288  
; EARLIER FILING DATE: 1998-04-01  
; EARLIER APPLICATION NUMBER: US 08/975, 080  
; EARLIER FILING DATE: 1997-11-20  
; EARLIER APPLICATION NUMBER: PCT/US97/21880  
; EARLIER FILING DATE: 1997-11-20  
; EARLIER APPLICATION NUMBER: US 60/031, 435  
; EARLIER FILING DATE: 1996-11-20  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 426  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Nucleotide sequence of open reading frame encoding  
; OTHER INFORMATION: Survivin  
US-09-283-144-2  
Alignment Scores:  
Pred. No.: 3,91e-141 Length: 426  
Score: 142.00 Matches: 142  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0

DB: 3 Gaps: 0

US-09-690-825-34 (1-142) x US-09-283-144-2 (1-426)

QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20

DB 1 ATGGGTGCCCCGAGCTGGCCCCCTGCTGGCAGGCCCTTTCTCAAGAGCCACCCGATCTCT 60

QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40

DB 61 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGGCCCTGCACCCCGGAGCGGATGGCCGAG 120

QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60

DB 121 GCTGCGTTCAATCCACTGCCCACTGAGACGAGCCAACTGGCCCACTTTCTTCTG 180

QY 61 PheLeuLysLeuGluGlyTrpGluProAspAspProIleGluGluHis 80

DB 181 TTCAAGAGCTGGAGGCTGGAGCCGACATGACACCCCAAGGAACTAAAGGCAAT 240

QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluLeuThrLeuGluGlu 100

DB 241 TCGTCCGTTGCGCTTCTTCTTCTGTCAGAGAGCTTTAAGAAATTAACCTTGGTGA 300

QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120

DB 301 TTTTGAAGACTGACAGAGAAAGAGCCAGCAAAATTCGAAAGGAAACCAATTAAG 360

QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGluLeuAlaAla 140

DB 361 AAGAAAGAAATTTGAGAACTGCGAAGAAAGTGGCGCTGCATCGAGCAGCTGGCTGCC 420

QY 141 MetAsp 142

DB 421 ATGGAT 426

RESULT 2

US-09-163-162-1

Sequence 1, Application US/09163162

Patent No. 6077709

GENERAL INFORMATION:

APPLICANT: Bennett, C. Frank

APPLICANT: Ackermann, Elizabeth J.

APPLICANT: Swayze, Eric E.

APPLICANT: Cowser, Lex M.

TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION

FILE REFERENCE: RTS-0008

CURRENT APPLICATION NUMBER: US/09/163,162

CURRENT FILING DATE: 1998-09-29

NUMBER OF SEQ ID NOS: 47

SEQ ID NO 1

LENGTH: 1619

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (50)..(478)

US-09-163-162-1

Alignment Scores:

Pred. No.: 1,35e-140 Length: 1619

Score: 142.00 Matches: 142

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

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DB 50 ATGGGTGCCCCGAGCTGGCCCCCTGCTGGCAGGCCCTTTCTCAAGAGCCACCCGATCTCT 109

QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40

DB 110 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGGCCCTGCACCCCGGAGCGGATGGCCGAG 169

QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60

DB 170 GCTGCGTTCAATCCACTGCCCACTGAGACGAGCCAGCTGGCCCGATGTTCTTCTG 229

QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHis 80

DB 230 TTCAAGAGCTGGAGGCTGGAGCCGACATACACCCCATAGAGAACTAAAGGCAAT 289

QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluLeuThrLeuGluGlu 100

DB 290 TCGTCCGTTGCGCTTCTTCTTCTGTCAGAGAGCTTTAAGAAATTAACCTTGGTGA 349

QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120

DB 350 TTTTGAAGACTGACAGAGAAAGAGCCAGCAAAATTCGAAAGGAAACCAATTAAG 409

QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGluLeuAlaAla 140

DB 410 AAGAAAGAAATTTGAGAACTGCGAAGAAAGTGGCGCTGCATCGAGCAGCTGGCTGCC 469

QY 141 MetAsp 142

DB 470 ATGGAT 475

RESULT 3

US-09-286-407-1

Sequence 1, Application US/09286407A

Patent No. 6165788

GENERAL INFORMATION:

APPLICANT: Bennett, C. Frank

APPLICANT: Ackermann, Elizabeth J.

APPLICANT: Swayze, Eric E.

APPLICANT: Cowser, Lex M.

TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION

FILE REFERENCE: ISPH-0349

CURRENT APPLICATION NUMBER: US/09/286,407A

CURRENT FILING DATE: 1999-04-05

NUMBER OF SEQ ID NOS: 48

SEQ ID NO 1

LENGTH: 1619

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (50)..(478)

US-09-286-407-1

Alignment Scores:

Pred. No.: 1,35e-140 Length: 1619

Score: 142.00 Matches: 142

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

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QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20

DB 50 ATGGGTGCCCCGAGCTGGCCCCCTGCTGGCAGGCCCTTTCTCAAGAGCCACCCGATCTCT 109

QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40

DB 110 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGGCCCTGCACCCCGGAGCGGATGGCCGAG 169

QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60

DB 170 GCTGCGTTCAATCCACTGCCCACTGAGACGAGCCAGCTGGCCCGATGTTCTTCTG 229

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QY 81 SerSeGlyCYsaAlaPheLeuSerValIlySlyGlnPheGluGluLeuThrIleuGlyGlu 100  
DB 290 TCGTCCGGGTGCCCCCTTCTCTGTCGAAGACAGCTTGAAGAAATTAACCTTGCTGAA 349  
QY 101 PheLeuLysLeuAspArgGluArgAlaIlyAsnLysIleAlaIlySGluThrAsnLys 120  
DB 350 TTTTGAACCTGACAGAGAAAGCCAGACAAATTCAGAAAGAAACCAACATTANG 409  
QY 121 LysLysGluPheGluGluGluThrAlaIlySlyValArgArgAlaIleGluGluLeuAla 140  
DB 410 AAGAAGAAATTTGAGAAACTGCGAAGAAAGTGCGCGCTGCATCGACAGCTGGCTGCC 469  
QY 141 MetAsp 142  
DB 470 ATGGAT 475  
RESULT 4  
US-09-496-694B-97  
; Sequence 97, Application US/09496694B  
; Patent No. 6335194  
; GENERAL INFORMATION:  
; APPLICANT: C. Frank Bennett  
; APPLICANT: Elizabeth J. Ackermann  
; APPLICANT: Eric E. Swayze  
; APPLICANT: Lex M. Comsart  
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION  
; FILE REFERENCE: ISPH-0439  
; CURRENT APPLICATION NUMBER: US/09/496,694B  
; CURRENT FILING DATE: 2000-02-02  
; PRIOR APPLICATION NUMBER: 09/286,407  
; PRIOR FILING DATE: 1999-04-05  
; PRIOR APPLICATION NUMBER: 09/163,162  
; PRIOR FILING DATE: 1998-09-29  
; NUMBER OF SEQ ID NOS: 249  
; SEQ ID NO 97  
; LENGTH: 1619  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-496-694B-97  
Alignment Scores:  
Pred. No.: 1,35e-140 Length: 1619  
Score: 142.00 Matches: 142  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
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DB 50 ATGGAGGCCCGCAGCTGGCCCTGCTGCAAGCCCTTTCTCAAGACACCGCATCTT 109  
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DB 170 GCTGGCTTATTCACATGCCCACTGAGACGACCACTGCGCCCAAGTTCCTTCTTCC 229  
QY 61 PheLysGluLeuGluGlyTTPGluProAspAspProIleGluGluHisIleSlySlySHS 80  
DB 230 TTCAAGAGAGCTGGAAGCTGGGAGCAGATGACGACCCCATAGAGAAACATAAAAGCAT 289  
QY 81 SerSeGlyCYsaAlaPheLeuSerValIlySlyGlnPheGluGluLeuThrIleuGlyGlu 100  
DB 290 TCGTCCGGGTGCCCCCTTCTCTGTCGAAGACAGCTTGAAGAAATTAACCTTGCTGAA 349

QY 101 PheLeuLysLeuAspArgGluArgAlaIlyAsnLysIleAlaIlySGluThrAsnLys 120  
DB 350 TTTTGAACCTGACAGAGAAAGCCAGACAAATTCAGAAAGAAACCAACATTANG 409  
QY 121 LysLysGluPheGluGluGluThrAlaIlySlyValArgArgAlaIleGluGluLeuAla 140  
DB 410 AAGAAGAAATTTGAGAAACTGCGAAGAAAGTGCGCGCTGCATCGACAGCTGGCTGCC 469  
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DB 470 ATGGAT 475  
RESULT 5  
US-08-448-722A-1/c  
; Sequence 1, Application US/08448722A  
; Patent No. 6072028  
; GENERAL INFORMATION:  
; APPLICANT: Altieri, Dario C.  
; TITLE OF INVENTION: No. 6072028e1 Cell Surface Receptor, Antibody  
; TITLE OF INVENTION: Compositions, and Methods of Using Same  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Office of Patent Counsel, The Scripps  
; STREET: Research Institute  
; STREET: 10550 No. 6072028th Torrey Pines Road, TPC-8  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: US  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/448,722A  
; FILING DATE: 25-MAY-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/189,309  
; FILING DATE: 28-JAN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitting, Thomas  
; REGISTRATION NUMBER: 34,163  
; REFERENCE/DOCKET NUMBER: 233.1 Div1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 784-2937  
; TELEFAX: (619) 784-9399  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1165 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 37..1047  
US-08-448-722A-1  
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Pred. No.: 8.7e-104 Length: 1165  
Score: 107.00 Matches: 138  
Percent Similarity: 99.28% Conservative: 0  
Best Local Similarity: 99.28% Mismatches: 1  
Query Match: 75.35% Indels: 1  
DB: 3 Gaps: 0  
US-09-690-825-34 (1-142) x US-08-448-722A-1 (1-1165)

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Db 1114 ATGGGTGCCCCGAGCTTGGCCCCCTGCTGGCAGCCCTTTTTCAGAGACCAACCCATCTCT 1055  
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40  
Db 1054 ACATTCAAGAACTGGCCCTTCTTGAGAGGCTGGCC-TGCACCCCGAGCGAGTGGCCGAG 996  
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60  
Db 995 GCTGGCTTCATCCACTGCCCACTGAGAGACGAGCCAGACTGGCCCAAGTGTTCCTTCG 936  
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis 80  
Db 935 TTCAAGAGAGCTGGAAGGCTGGAGCCAGATGACGACCCCAAGAGAACATAAAGCAT 876  
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100  
Db 875 TCGCCCGGTTGCGCTTCTTCTGTCAGAGACAGTTGAAGATTAAACCTTGATGA 816  
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120  
Db 815 TTTTGAACTGGACAGAGAAAGGCCAAGAACAAATTCCAAAGAAACCAACATTAAG 756  
QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAla 139  
Db 755 AAGAAAGATTGTGAGAACTGCGAAGAAAGTGCGCGCTGCCATCGAGAGCTGGCC 699

RESULT 6  
US-08-189-309B-1/C  
Sequence 1, Application US/08189309B  
Patent No. 6238875  
GENERAL INFORMATION:  
APPLICANT: Altieri, Darío C.  
TITLE OF INVENTION: Diagnostic Methods Useful in the Characterization of  
TITLE OF INVENTION: Lymphoproliferative Disease Characterized by Increased EPR-1  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Office of Patent Counsel, The Scripps  
ADDRESSER: Research Institute  
STREET: 10550 No. 6238875th Torrey Pines Road, TPC-8  
CITY: La Jolla  
STATE: CA  
COUNTRY: US  
ZIP: 92037

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/189,309B  
FILING DATE: 28-JAN-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,897  
FILING DATE: 10-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/667,957  
FILING DATE: 12-MAR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: 233.1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 784-2937  
TELEFAX: (619) 784-9399  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1165 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 37..1047  
US-08-189-309B-1

Alignment Scores:  
Pred. No.: 8.76-104  
Score: 107.00  
Percent Similarity: 99.28%  
Best Local Similarity: 99.28%  
Query Match: 75.35%  
Caps: 3

US-09-690-825-34 (1-142) x US-08-189-309B-1 (1-1165)

QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20  
Db 1114 ATGGGTGCCCCGAGCTTGGCCCCCTGCTGGCAGCCCTTTTTCAGAGACCAACCCATCTCT 1055  
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40  
Db 1054 ACATTCAAGAACTGGCCCTTCTTGAGAGGCTGGCC-TGCACCCCGAGCGAGTGGCCGAG 996  
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60  
Db 995 GCTGGCTTCATCCACTGCCCACTGAGAGACGAGCCAGACTGGCCCAAGTGTTCCTTCG 936  
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis 80  
Db 935 TTCAAGAGAGCTGGAAGGCTGGAGCCAGATGACGACCCCAAGAGAACATAAAGCAT 876  
QY 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100  
Db 875 TCGCCCGGTTGCGCTTCTTCTGTCAGAGACAGTTGAAGATTAAACCTTGATGA 816  
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120  
Db 815 TTTTGAACTGGACAGAGAAAGGCCAAGAACAAATTCCAAAGAAACCAACATTAAG 756  
QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGlnLeuAla 139  
Db 755 AAGAAAGATTGTGAGAACTGCGAAGAAAGTGCGCGCTGCCATCGAGAGCTGGCC 699

RESULT 7  
US-09-016-434-918  
Sequence 918, Application US/09016434  
Patent No. 6500938  
GENERAL INFORMATION:  
APPLICANT: Jeffrey J. Seilhamer  
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
NUMBER OF SEQUENCES: 1490  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/016,434  
FILING DATE: HERWITH  
CLASSIFICATION:  
PRIOR APPLICATION DATA:

APPLICATION NUMBER:  
 FILING DATE:  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Zeller, Karen J.  
 REGISTRATION NUMBER: 37,071  
 REFERENCE/DOCKET NUMBER: PA-0002 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (650) 855-0555  
 TELEFAX: (650) 845-4166  
 INFORMATION FOR SEQ ID NO: 918:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 740 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 IMMEDIATE SOURCE:  
 LIBRARY: BRAITUT01  
 CLONE: 752848  
 US-09-016-434-918

Alignment Scores:  
 Pred. No.: 3,41e-89 Length: 740  
 Score: 93.00 Matches: 130  
 Percent Similarity: 98.48% Conservative: 0  
 Best Local Similarity: 98.48% Mismatches: 1  
 Query Match: 65.49% Indels: 2  
 DB: Gaps: 0

US-09-690-825-34 (1-142) x US-09-016-434-918 (1-740)

QY 12 ProPheLeuLysAspHisArgIleSerThrPheLysAsnTTPProPheLeuGluGlyCys 31  
 Db 51 CCTTTCTCAAGAGACCCGACCTCTTACATTCAGAACTGGCCCTTCTTGAGGGCTGC 110  
 QY 32 AlaCysThrProGluArgMetAlaGluAlaGlyPheIleHisCysAspProThrGlu-AsnG 51  
 Db 111 GCCTGCACCCCGAGGGAGGAGCGCGGCTGCTTATCCATCGCCCACTGA-NACGA 169  
 QY 51 uPcOAspLeuAlaGluCysPhePheCysPheLysGluLeuGluGlyTTPGluProAspAs 71  
 Db 170 GCCAGACTTGCCCAAGTCTTCTTCTGCTTCAAGAGCTGGAGAGGCTGGAGCCAGATA 229  
 QY 71 PAAPProIleGluGluHisLysLysHisSerSerGlyCysAlaPheLeuSerValLysLys 91  
 Db 230 CGACCCCATAGAGAAACATATAAGCATTCGTCGGTGGCTTCTTCTGTCAGAA 289  
 QY 91 sGlnPheGluGluLeuThrLeuGluGluPheLeuLysAspArgGluArgAlaLysAs 111  
 Db 290 GCGATTGGAAGATTAACTTGTGTGATTTTGAACCTGACAGAGAAAGAGCCAAAGA 349  
 QY 111 nLysIleAlaLysGluThrAsnAsnLysLysLysGluPheGluGluThrAlaLysLysVa 131  
 Db 350 CAAATATGCAAGGAAACCAACATATAAGAAAGAAATTGAGAGAAATCGCAAGAAAG 409  
 QY 131 lArgArgAlaIleGluGluLeuAlaAlaMetasp 142  
 Db 410 GCGCGCTGCATGAGCAGCTGCTGCCATGAT 443

# RESULT 8

US-09-513-999C-2315  
 ; Sequence 2315, Application US/09513999C  
 ; Patent No. 6783961  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dumas Milne Edwards, J.B.  
 ; APPLICANT: Duclert, A.  
 ; APPLICANT: Giordano, J.Y.  
 ; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
 ; Patent No. 6783961  
 ; FILE REFERENCE: 59.US2.REG  
 ; CURRENT APPLICATION NUMBER: US/09/513,999C  
 ; CURRENT FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: US 60/122,487

PRIOR FILING DATE: 1999-02-26  
 ; NUMBER OF SEQ ID NOS: 36681  
 ; SOFTWARE: Patent.pm  
 ; SEQ ID NO 2315  
 ; LENGTH: 399  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 52..399  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: 32  
 ; OTHER INFORMATION: k=g or t  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: 279  
 ; OTHER INFORMATION: r=a or g  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: 280  
 ; OTHER INFORMATION: s=g or c  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: 318  
 ; OTHER INFORMATION: s=g or c  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: 342  
 ; OTHER INFORMATION: s=g or c  
 ; FEATURE:  
 ; NAME/KEY: UNSURE  
 ; LOCATION: 77  
 ; OTHER INFORMATION: Xaa=asp or His  
 ; US-09-513-999C-2315

Alignment Scores:  
 Pred. No.: 1.68e-71 Length: 399  
 Score: 76.00 Matches: 115  
 Percent Similarity: 98.29% Conservative: 0  
 Best Local Similarity: 98.29% Mismatches: 1  
 Query Match: 53.52% Indels: 2  
 DB: Gaps: 0

US-09-690-825-34 (1-142) x US-09-513-999C-2315 (1-399)

QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20  
 Db 52 ATGGGTGCCCCGAGAGTTCCTCCCTGCGAGCCCTTCTCAAGAGACCCGACATCTCT 111  
 QY 21 ThrPheLysAsnTTPProPheLeuGluGlyCysAlaCysTTPProGluArgMetAlaGlu 40  
 Db 112 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGCGCTGACCCCGAGAGGAGTGGCGAG 171  
 QY 41 AlaGlyPheIleHisCysPProThrGluGluGluPheLeuAlaGluCysPhePheCys 60  
 Db 172 GCTGCTTCATCCACTGCCCCCACTGAGACAGCAGACTTGCCCAAGTGTCTTCTGCC 231  
 QY 61 PheLysGluLeuGluGlyTTPGluProAspAspProIleGluGluHis-LysLysHis 80  
 Db 232 TTCAGAGAGCTGGAAGGCTGGAGGCAAGTACGACCCCATAGAGARSA-TAAGAAACA 290  
 QY 80 sSerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyG 100  
 Db 291 TTCGTCGGCTTGCGCTTCTTCTTCTGTAAGAGAGCTTGAAGATTAACGCTTGATGA 350  
 QY 100 uPheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGlu 116  
 Db 351 ATTTTGAAGACTGACAGAGAAAGAGCCAAAGAAATTCAGAAAGAA 399

# RESULT 9

US-09-496-694B-10  
 ; Sequence 10, Application US/09496694B

Patent No. 6335194  
GENERAL INFORMATION:  
APPLICANT: C. Frank Bennett  
APPLICANT: Elizabeth J. Ackermann  
APPLICANT: Eric E. Swazey  
APPLICANT: Lex M. Cowsett  
TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION  
FILE REFERENCE: ISPH-0439  
CURRENT APPLICATION NUMBER: US/09/496,694B  
CURRENT FILING DATE: 2000-02-02  
PRIOR APPLICATION NUMBER: 09/266,407  
PRIOR FILING DATE: 1999-04-05  
PRIOR APPLICATION NUMBER: 09/163,162  
PRIOR FILING DATE: 1998-09-29  
NUMBER OF SEQ ID NOS: 249  
SEQ ID NO 10  
LENGTH: 955  
TYPE: DNA  
ORGANISM: Mus musculus  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (109)...(531)  
US-09-496-694B-10

Alignment Scores:  
Pred. No.: 3,32e-34 Length: 955  
Score: 41.00 Matches: 41  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 28.87% Indels: 0  
Gaps: 0

US-09-690-825-34 (1-142) x US-09-496-694B-10 (1-955)

QY 31 CysAlaCyThrProGluArgMetAlaGluAlaGlyPheIleHisCysPProThrGluAsn 50  
Db 199 TGCCCTCGCCACCCGAGCGCGATGCGAGGCTGCTTCATCCACCTACCGAGAAC 258

QY 51 GluProAspLeuAlaGlnCysPhePheCysPheIleGluGlyTTPGluProAsp 70  
Db 259 GAGCTGATTTGGCCGACGTTTCTGCTTTAAGAAATTGGAGAGGCTGGAAACCGAT 318

QY 71 Asp 71  
Db 319 GAC 321

RESULT 10  
US-08-975-080-35  
Sequence 35, Application US/08975080  
Patent No. 6245523  
GENERAL INFORMATION:  
APPLICANT: Altieri, Dario C.  
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS  
CELLULAR APOPTOSIS, AND ITS MODULATION  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP  
STREET: 1800 M Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20036-5869  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/975,080  
FILING DATE: 20-NOV-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/031,435  
FILING DATE: 20-NOV-1996

ATTORNEY/AGENT INFORMATION:  
NAME: Adler, Reid G.  
REGISTRATION NUMBER: 30,988  
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-467-7000  
TELEFAX: 202-467-7176  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14796 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-975-080-35

Alignment Scores:  
Pred. No.: 5.48e-31 Length: 14796  
Score: 39.00 Matches: 39  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 27.46% Indels: 0  
Gaps: 0

US-09-690-825-34 (1-142) x US-08-975-080-35 (1-14796)

QY 75 GluGluHisLysLysHisSerSerGlyCysAlaPheLeuSerValLysLysGlnPheGlu 94  
Db 5159 GAGGAACATAAAAGACATTCCTCCGTTGCCCTTCTTGTGCAAGAACACTTGAA 5218

QY 95 GluLeuThrLeuGlyGluPheLeuLysLeuAspArgLysArgAlaLysAsnLysIle 113  
Db 5219 GAATTAACCTTGGTGAATTTTGAACCTGACAGAAAGACCAAGACCAAAATT 5275

RESULT 11  
US-09-630-706-10  
Sequence 10, Application US/09630706  
Patent No. 6277640  
GENERAL INFORMATION:  
APPLICANT: C. Frank Bennett  
TITLE OF INVENTION: ANTISENSE MODULATION OF HER-3 EXPRESSION  
FILE REFERENCE: RTS-0053  
CURRENT APPLICATION NUMBER: US/09/630,706  
CURRENT FILING DATE: 2000-08-01  
NUMBER OF SEQ ID NOS: 94  
SEQ ID NO 10  
LENGTH: 14796  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (2811)...(2921)  
NAME/KEY: CDS  
LOCATION: (3174)...(3283)  
NAME/KEY: CDS  
LOCATION: (5158)...(5275)  
NAME/KEY: CDS  
LOCATION: (11955)...(12044)  
US-09-630-706-10

Alignment Scores:  
Pred. No.: 5.48e-31 Length: 14796  
Score: 39.00 Matches: 39  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 27.46% Indels: 0  
Gaps: 0

US-09-690-825-34 (1-142) x US-09-630-706-10 (1-14796)

QY 75 GluGluHisLysLysHisSerSerGlyCysAlaPheLeuSerValLysLysGlnPheGlu 94  
|||||



Db 5159 GAGGAAACATATAAAGCATTCGTCGGCTTCCTTCCTTCGTCAGAGAGCATTTGAA 5218  
Qy 95 GtluLeuThrluGlyGluPheLeuLysLeuAspArgGluArgAlaLysAsnLysIle 113  
Db 5219 GAATTACCTTCGTCGTAATTTTGGAAACTGGACAGAAAGGCCAAGACAAATTT 5275  
RESULT 12  
US-09-496-694B-3  
; Sequence 3, Application US/09496694B  
; Patent No. 6335194  
; GENERAL INFORMATION:  
; APPLICANT: C. Frank Bennett  
; APPLICANT: Elizabeth J. Ackermann  
; APPLICANT: Eric B. Swayze  
; APPLICANT: Lex M. Cowser  
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION  
; FILE REFERENCE: ISPH-0439  
; CURRENT APPLICATION NUMBER: US/09/496,694B  
; CURRENT FILING DATE: 2000-02-02  
; PRIOR APPLICATION NUMBER: 09/286,407  
; PRIOR FILING DATE: 1998-04-05  
; PRIOR APPLICATION NUMBER: 09/163,162  
; PRIOR FILING DATE: 1998-09-29  
; NUMBER OF SEQ ID NOS: 249  
; SEQ ID NO 3  
; LENGTH: 14796  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (2811) ... (2921)  
; NAME/KEY: CDS  
; LOCATION: (3174) ... (3283)  
; NAME/KEY: CDS  
; LOCATION: (5158) ... (5275)  
; NAME/KEY: CDS  
; LOCATION: (11955) ... (12044)  
US-09-496-694B-3  
Alignment Scores:  
Pred. No.: 5,48e-31 Length: 14796  
Score: 39.00 Matches: 39  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 27.46% Indels: 0  
Gaps: 0  
US-09-690-825-34 (1-142) x US-09-496-694B-3 (1-14796)  
Qy 75 GtluGluHslLysLysHisSerSergLysAlaPheLeuSerValLysLysGlnPheGlu 94  
Db 5159 GAGGAAACATATAAAGCATTCGTCGGCTTCCTTCCTTCGTCAGAGAGCATTTGAA 5218  
Qy 95 GtluLeuThrluGlyGluPheLeuLysLeuAspArgGluArgAlaLysAsnLysIle 113  
Db 5219 GAATTACCTTCGTCGTAATTTTGGAAACTGGACAGAAAGGCCAAGACAAATTT 5275  
RESULT 13  
US-09-283-144-1  
; Sequence 1, Application US/09283144  
; Patent No. 6346389  
; GENERAL INFORMATION:  
; APPLICANT: Yale University  
; TITLE OF INVENTION: Method for Selectively Modulating the Interactions  
; TITLE OF INVENTION: between Survivin and Tubulin  
; FILE REFERENCE: 44574-5033-US  
; CURRENT APPLICATION NUMBER: US/09/283,144  
; CURRENT FILING DATE: 1998-04-01  
; EARLIER APPLICATION NUMBER: US 60/080,288  
; EARLIER FILING DATE: 1998-04-01  
; EARLIER APPLICATION NUMBER: US 08/975,080  
; EARLIER FILING DATE: 1997-11-20  
; EARLIER APPLICATION NUMBER: PCT/US97/21880.

; EARLIER FILING DATE: 1997-11-20  
; EARLIER APPLICATION NUMBER: US 60/031,435  
; EARLIER FILING DATE: 1996-11-20  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 417  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: DNA sequence of proximal 5' flanking region of  
; OTHER INFORMATION: Survivin gene  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (291) .. (401)  
US-09-283-144-1  
Alignment Scores:  
Pred. No.: 2.56e-30 Length: 417  
Score: 37.00 Matches: 37  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 26.06% Indels: 0  
Gaps: 0  
US-09-690-825-34 (1-142) x US-09-283-144-1 (1-417)  
Qy 1 MetGlyAlaProThrLeuProProAlaTyrGlnProPheLeuLysAspHisArgIleSer 20  
Db 291 ATGGGTGCCCGAGAGTTCCTGCTGCGAGCCCTTCTTCAAGAGACCGCATCTCT 350  
Qy 21 ThrPheLysAsnTyrProPheLeuGluGlyCysAlaCysThrProGluArg 37  
Db 351 ACATTCAAGAACTGGCCCTTCTTGAGAGGCTGCGCCTGACCCCGGAGCGG 401  
RESULT 14  
US-09-672-717-199  
; Sequence 199, Application US/09672717  
; Patent No. 6673917  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G.  
; APPLICANT: Lacasse, Eric  
; APPLICANT: Baird, Stephen  
; APPLICANT: Holcik, Martin  
; APPLICANT: Young, Sean  
; TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses  
; FILE REFERENCE: 07891/025001  
; CURRENT APPLICATION NUMBER: US/09/672,717  
; CURRENT FILING DATE: 2000-09-28  
; NUMBER OF SEQ ID NOS: 231  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 199  
; LENGTH: 30  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: based on Homo sapiens  
US-09-672-717-199  
Alignment Scores:  
Pred. No.: 0.079 Length: 30  
Score: 9.00 Matches: 9  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 6.34% Indels: 0  
Gaps: 0  
US-09-690-825-34 (1-142) x US-09-672-717-199 (1-30)  
Qy 69 ProAspAspProIleGluGluHis 77  
Db 3 CCGATGAGACCCCATAGAGAAACAT 29

```
RESULT 15
US-09-496-694B-13
; Sequence 13, Application US/09496694B
; Patent No. 6335194
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Eric E. Swayze
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: ISPH-0439
; CURRENT APPLICATION NUMBER: US/09/496,694B
; CURRENT FILING DATE: 2000-02-02
; PRIOR APPLICATION NUMBER: 09/286,407
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 09/163,162
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 249
; SEQ ID NO 13
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Probe
US-09-496-694B-13

Alignment Scores:
Pred. No.:      0.786      Length:      26
Score: '      8.00      Matches:      8
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      5.63%      Indels:      0
DB:      3      Gaps:      0

US-09-690-825-34 (1-142) x US-09-496-694B-13 (1-26)

QY      62  LysGluLeuGluGlyTyrGluPro 69
      |||||
Db      2  AAGCAATTGGAGAGGCTGGGAACCC 25

Search completed: November 1, 2004, 20:33:50
Job time : 97 secs
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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 1, 2004, 19:10:41 ; Search time 369 Seconds

(without alignments)  
1973.223 Million cell updates/sec

Title: US-09-690-825-34

Perfect score: 778  
Sequence: 1 MCAPPLPPAMOPFLMDHRIS.....EFEETAKVRAIQALAMD 142

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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3413475 segs, 2563800928 residues

Total number of hits satisfying chosen parameters: 6826950

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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-O/cgnt2\_1/USPTO.spool/p/US09690825/rnatc.0112004.105431.1918/app.query.fasta.1.327  
-DB=Published Applications NA -QEXT=fastap -SUFFIX=trmpb -MIMATCH=0.1  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=0.001 -THR MAX=100  
-THR\_MIN=0 -ALIGN=15 -XGAP=100 -XGAPEXT=100 -XGAPOP=100 -XGAPEXT=100  
-MAXLEN=2000000000 -MAP=LARGOQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100  
-NCPU=6 -ICPU=3 -NO MAP -LARGOQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100  
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database:

Published Applications NA:  
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2: /cgnt2\_6/prodata/1/pubpna/PCT\_NEW\_PUB.seq:  
3: /cgnt2\_6/prodata/1/pubpna/US06\_PUBCOMB.seq:  
4: /cgnt2\_6/prodata/1/pubpna/US07\_NEW\_PUB.seq:  
5: /cgnt2\_6/prodata/1/pubpna/US08\_PUBCOMB.seq:  
6: /cgnt2\_6/prodata/1/pubpna/US09\_PUBCOMB.seq:  
7: /cgnt2\_6/prodata/1/pubpna/US08\_NEW\_PUB.seq:  
8: /cgnt2\_6/prodata/1/pubpna/US08\_PUBCOMB.seq:  
9: /cgnt2\_6/prodata/1/pubpna/US09\_PUBCOMB.seq:  
10: /cgnt2\_6/prodata/1/pubpna/US09\_PUBCOMB.seq:  
11: /cgnt2\_6/prodata/1/pubpna/US09\_NEW\_PUB.seq:  
12: /cgnt2\_6/prodata/1/pubpna/US09\_PUBCOMB.seq:  
13: /cgnt2\_6/prodata/1/pubpna/US10\_PUBCOMB.seq:  
14: /cgnt2\_6/prodata/1/pubpna/US10\_PUBCOMB.seq:  
15: /cgnt2\_6/prodata/1/pubpna/US10\_PUBCOMB.seq:  
16: /cgnt2\_6/prodata/1/pubpna/US10\_PUBCOMB.seq:  
17: /cgnt2\_6/prodata/1/pubpna/US10\_PUBCOMB.seq:  
18: /cgnt2\_6/prodata/1/pubpna/US10\_PUBCOMB.seq:  
19: /cgnt2\_6/prodata/1/pubpna/US11\_NEW\_PUB.seq:  
20: /cgnt2\_6/prodata/1/pubpna/US60\_NEW\_PUB.seq:  
21: /cgnt2\_6/prodata/1/pubpna/US60\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	778	100.0	429	17	US-10-665-975-1
2	778	100.0	1619	9	US-09-918-186A-97
3	778	100.0	1619	15	US-10-181-316-97
4	778	100.0	1619	15	US-10-172-118-566
5	778	100.0	1619	15	US-10-388-360-324
6	778	100.0	1619	15	US-10-342-887-566
7	778	100.0	1619	16	US-10-283-975A-445
8	778	100.0	1619	17	US-10-657-022-99
9	778	100.0	1619	17	US-10-807-897-1
10	778	100.0	2404	13	US-10-071-766-109
11	778	100.0	2404	15	US-10-084-817-285
12	772	99.2	2570	17	US-10-741-601-210
13	772	99.2	2585	17	US-10-741-601-215
14	750.5	96.5	2639	17	US-10-741-601-215
15	750.5	96.5	2654	17	US-10-741-601-211
16	721	92.7	740	16	US-10-305-720-918
17	660	84.8	955	9	US-09-918-186A-10
18	660	84.8	955	15	US-10-181-316-10
19	638	82.0	955	18	US-10-807-897-3
20	525.5	67.5	578	17	US-10-741-601-213
21	525.5	67.5	2452	17	US-10-741-601-212
22	525.5	67.5	2467	17	US-10-741-601-214
23	382	49.1	14795	15	US-10-181-316-3
24	382	49.1	14796	9	US-09-954-456-973
25	382	49.1	14796	9	US-09-954-456-1636
26	382	49.1	14796	9	US-09-918-186A-3
27	382	49.1	14796	9	US-09-880-107-3421
28	382	49.1	14796	11	US-09-968-007A-5522
29	382	49.1	14796	15	US-10-138-618-35
30	382	49.1	23393	17	US-10-741-601-5680
31	382	49.1	41339	17	US-10-741-601-5768
32	347	44.6	332	9	US-09-833-381-1331
33	298	38.3	555	15	US-10-029-386-9972
34	233	28.7	121	15	US-10-179-730-33
35	223	28.7	201	17	US-10-741-601-4404
36	223	28.7	201	17	US-10-741-601-4415
37	223	28.7	201	17	US-10-741-601-4451
38	223	28.7	201	17	US-10-741-601-4462
39	216	27.8	120	15	US-10-029-386-23672
40	214	27.5	1100	14	US-10-108-877-2
41	211	27.1	378	17	US-10-430-201-2114
42	211	27.1	378	17	US-10-430-201-2115
43	201.5	25.9	201	17	US-10-741-601-4427
44	201.5	25.9	201	17	US-10-741-601-4439
45	155	19.9	5502	16	US-10-641-643-1459

## ALIGNMENTS

RESULT 1  
US-10-665-975-1  
Sequence 1, Application US/10665975  
Publication No. US2004038119A1  
GENERAL INFORMATION:  
APPLICANT: Reed, John C.  
TITLE OF INVENTION: USE OF HEPATITIS VIRUS B X-INTERACTING  
TITLE OF INVENTION: PROTEIN (HEXIP) IN MODULATION OF APOPTOSIS  
FILE REFERENCE: BURNHAM.005A  
CURRENT APPLICATION NUMBER: US/10/665,975  
PRIOR FILING DATE: 2003-09-18  
PRIOR APPLICATION NUMBER: 60/412,109  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 429  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-665-975-1

## Alignment Scores:

Pred. No.: 1.7e-93 Length: 429  
 Score: 778.00 Matches: 142  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 17 Gaps: 0

US-09-690-825-34 (1-142) x US-10-665-975-1 (1-429)

QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20  
 DB 1 ATGGAGTGGCCCGAGCTGAGCTGCTGCTGAGCCCTTTCTCAAGAGCCACCGCATCTCT 60  
 QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40  
 DB 61 ACATTCAAGAACTGGCCCTTTCTTGGAGGGCTGCGCCCTGACCCCGGAGCGGATGGCCGAG 120  
 QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60  
 DB 121 GCTGCTTCATCCACTGCTCCCATGAGACGAGCCACACTTGGCCCATGTTCTTCTTCTG 180  
 QY 61 PheLysGluLeuGluGlyTrpGluProAspAspAspProIleGluGluHisLysLysHis 80  
 DB 181 TTCAAGAGAGCTGGAGAGCTGGAGCCAGATGACGACCCCATAGAGACATATAAAGCAT 240  
 QY 81 SerSerGlyCysAlaPheLeuSerValLysGlnPheGluGluLeuThrLeuGluGlu 100  
 DB 241 TCGTCCGCTTGGCTTCTTCTTCTGTAAGAGACAGTTTAAAGATTAACTTGTGTGA 300  
 QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120  
 DB 301 TTTTGAACCTGGACAGAGAGAGCCAGCAAAATTCAAGAGAAACCAACATTAAG 360  
 QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGluLeuAlaIle 140  
 DB 361 AAGAAAGATTGAGAGAACTGGAGAGAAAGTGGCGCTGCTCAAGAGCTGCTGCC 420  
 QY 141 MetAsp 142  
 DB 421 ATGGAT 426

## RESULT 2

US-09-918-186A-97  
 ; Sequence 97, Application US/09918186A  
 ; Patent No. US20020137708A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: C. Frank Bennett  
 ; APPLICANT: Elizabeth J. Ackermann  
 ; APPLICANT: Eric E. Swayze  
 ; APPLICANT: Lex M. Cowse  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION  
 ; FILE REFERENCE: ISPH-0585  
 ; CURRENT APPLICATION NUMBER: US/09/918,186A  
 ; PRIOR FILING DATE: 2001-07-30  
 ; PRIOR APPLICATION NUMBER: 09/496,694  
 ; PRIOR FILING DATE: 2000-02-02  
 ; PRIOR APPLICATION NUMBER: 09/286,407  
 ; PRIOR FILING DATE: 1999-04-05  
 ; PRIOR APPLICATION NUMBER: 09/163,162  
 ; PRIOR FILING DATE: 1998-09-29  
 ; NUMBER OF SEQ ID NOS: 250  
 ; SEQ ID NO 97  
 ; LENGTH: 1619  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-918-186A-97

## Alignment Scores:

Pred. No.: 1.04e-92 Length: 1619  
 Score: 778.00 Matches: 142  
 Percent Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 15 Gaps: 0

Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0

US-09-690-825-34 (1-142) x US-09-918-186A-97 (1-1619)

QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20  
 DB 50 ATGGAGTGGCCCGAGCTGAGCTGCTGCTGAGCCCTTTCTCAAGAGCCACCGCATCTCT 109  
 QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40  
 DB 110 ACATTCAAGAACTGGCCCTTTCTTGGAGGGCTGCGCCCTGACCCCGGAGCGGATGGCCGAG 169  
 QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60  
 DB 170 GCTGCTTCATCCACTGCTCCCATGAGACGAGCCAGCTTGGCCCATGTTCTTCTG 229  
 QY 61 PheLysGluLeuGluGlyTrpGluProAspAspAspProIleGluGluHisLysLysHis 80  
 DB 230 TTCAAGAGAGCTGGAGAGCTGGAGCCAGATGACGACCCCATAGAGACATATAAAGCAT 285  
 QY 81 SerSerGlyCysAlaPheLeuSerValLysGlnPheGluGluLeuThrLeuGluGlu 100  
 DB 230 TCGTCCGCTTGGCTTCTTCTTCTGTAAGAGACAGTTTAAAGATTAACTTGTGTGA 349  
 QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120  
 DB 350 TTTTGAACCTGGACAGAGAGAGCCAGCAAAATTGAGAGAGAAACCAACATTAAG 409  
 QY 121 LysLysGluPheGluGluThrAlaLysLysValArgArgAlaIleGluGluLeuAlaIle 140  
 DB 410 AAGAAAGATTGAGAGAACTGGAGAGAAAGTGGCGCTGCTCAAGAGCTGCTGCC 469  
 QY 141 MetAsp 142  
 DB 470 ATGGAT 475

## RESULT 3

US-10-181-316-97  
 ; Sequence 97, Application US/10181316  
 ; Publication No. US20030211607A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: C. Frank Bennett  
 ; APPLICANT: Elizabeth J. Ackermann  
 ; APPLICANT: Eric E. Swayze  
 ; APPLICANT: Lex M. Cowse  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION  
 ; FILE REFERENCE: ISPH-0650  
 ; CURRENT APPLICATION NUMBER: US/10/181,316  
 ; PRIOR FILING DATE: 2002-07-16  
 ; PRIOR APPLICATION NUMBER: PCT/US01/02939  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: 09/496,694  
 ; PRIOR FILING DATE: 2000-02-02  
 ; PRIOR APPLICATION NUMBER: 09/286,407  
 ; PRIOR FILING DATE: 1999-04-05  
 ; PRIOR APPLICATION NUMBER: 09/163,162  
 ; PRIOR FILING DATE: 1998-09-29  
 ; NUMBER OF SEQ ID NOS: 249  
 ; SEQ ID NO 97  
 ; LENGTH: 1619  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-10-181-316-97

## Alignment Scores:

Pred. No.: 1.04e-92 Length: 1619  
 Score: 778.00 Matches: 142  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 15 Gaps: 0

US-09-690-825-34 (1-142) x US-10-181-316-97 (1-1619)

QY 1 MetGlyAlaProThrLeuProProAlaTTPGlnProPheLeuYsAspHisArgIleSer 20  
Db 50 ATGGGTGCCCCGACGCTTGCCCTTCTGCAAGACACCGCATCTCT 109

QY 21 ThrPheYsAsnTPProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40  
Db 110 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGCGCTGCACCCCGAGCGGATGGCCGAG 169

QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60  
Db 170 GCTGGCTTCATCCACTGCCCCCTGAGAACGACCACTGGCCCAAGTGTCTTCTTGC 229

QY 61 PheYsGluLeuGluGlyTTPGluProAspAspProIleGluGluHisIleSlySlyHis 80  
Db 230 TTCAAGAGCTGGAAAGCTGGGAGCGACATGACGCCCATGAGGAACTATAAAGCAT 289

QY 81 SerSerGlyCysAlaPheLeuSerValIleSlySlyGlnPheGluGluLeuThrLeuGlyGlu 100  
Db 290 TCGTCCGCTTGCGCTTCTTCTTCTGCAAGACACTTTGAAGATTAACTTGTGTA 349

QY 101 PheLeuYsLeuAspArgGluArgAlaIleYsAsnIleAlaIleYsGluThrAsnSlySly 120  
Db 350 TTTTGAAACTGGACACAGAAAGAGCCAAATAATGCAAGGAAACCAACATTAAG 409

QY 121 LysIleGluPheGluGluThrAlaIleYsValArgArgAlaIleGluGluLeuAlaIle 140  
Db 410 AAGAAAGAAATTGAGAAAGCTGGAAAGAGTGCCTGCTCATGAGCACTGGCTGCC 469

QY 141 MetAsp 142  
Db 470 ATGGAT 475

RESULT 4  
US-10-172-118-566  
; Sequence 566, Application US/10172118  
; Publication No. US20030224374A1  
; GENERAL INFORMATION:  
; APPLICANT: Dai, Hongyue  
; APPLICANT: He, Yudong  
; APPLICANT: Linsley, Peter  
; APPLICANT: Mao, Mao  
; APPLICANT: Roberts, Chris  
; APPLICANT: Van 't Veer, Laura  
; APPLICANT: Van de Vijver, Marc  
; APPLICANT: Bernards, Rene  
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients  
; FILE REFERENCE: 9301-175-999  
; CURRENT APPLICATION NUMBER: US/10/172,118  
; CURRENT FILING DATE: 2002-06-14  
; PRIOR APPLICATION NUMBER: 60/380,770  
; PRIOR FILING DATE: 2002-05-14  
; NUMBER OF SEQ ID NOS: 2659  
; SEQ ID NO 566  
; LENGTH: 1619  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: NM\_001168  
; DATABASE ENTRY DATE: 2001-06-18  
US-10-172-118-566

Alignment Scores:  
Pred. No.: 1,04e-92 Length: 1619  
Score: 778.00 Matches: 142  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 15 Gaps: 0

US-09-690-825-34 (1-142) x US-10-172-118-566 (1-1619)

QY 1 MetGlyAlaProThrLeuProProAlaTTPGlnProPheLeuYsAspHisArgIleSer 20  
Db 50 ATGGGTGCCCCGACGCTTGCCCTTCTGCAAGACACCGCATCTCT 109

QY 21 ThrPheYsAsnTPProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40  
Db 110 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGCGCTGCACCCCGAGCGGATGGCCGAG 169

QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60  
Db 170 GCTGGCTTCATCCACTGCCCCCTGAGAACGACCACTGGCCCAAGTGTCTTCTTGC 229

QY 61 PheYsGluLeuGluGlyTTPGluProAspAspProIleGluGluHisIleSlySlyHis 80  
Db 230 TTCAAGAGCTGGAAAGCTGGGAGCGACATGACGCCCATGAGGAACTATAAAGCAT 289

QY 81 SerSerGlyCysAlaPheLeuSerValIleSlySlyGlnPheGluGluLeuThrLeuGlyGlu 100  
Db 290 TCGTCCGCTTGCGCTTCTTCTTCTGCAAGACACTTTGAAGATTAACTTGTGTA 349

QY 101 PheLeuYsLeuAspArgGluArgAlaIleYsAsnIleAlaIleYsGluThrAsnSlySly 120  
Db 350 TTTTGAAACTGGACACAGAAAGAGCCAAATAATGCAAGGAAACCAACATTAAG 409

QY 121 LysIleGluPheGluGluThrAlaIleYsValArgArgAlaIleGluGluLeuAlaIle 140  
Db 410 AAGAAAGAAATTGAGAAAGCTGGAAAGAGTGCCTGCTCATGAGCACTGGCTGCC 469

QY 141 MetAsp 142  
Db 470 ATGGAT 475

RESULT 5  
US-10-388-360-324  
; Sequence 324, Application US/10388360  
; Publication No. US20030225528A1  
; GENERAL INFORMATION:  
; APPLICANT: GENOMIC HEALTH  
; APPLICANT: Baker, Joffie B.  
; APPLICANT: Cronin, Maureen T.  
; APPLICANT: Kiefer, Michael C.  
; APPLICANT: Shak, Steve  
; APPLICANT: Walker, Michael Graham  
; TITLE OF INVENTION: GENE EXPRESSION PROFILING IN BIOPSYED TUMOR TISSUES  
; FILE REFERENCE: 39740-0001US  
; CURRENT APPLICATION NUMBER: US/10/388,360  
; CURRENT FILING DATE: 2003-03-12  
; PRIOR APPLICATION NUMBER: US 60/412,049  
; PRIOR FILING DATE: 2002-09-18  
; PRIOR APPLICATION NUMBER: US 60/364,890  
; PRIOR FILING DATE: 2002-03-13  
; NUMBER OF SEQ ID NOS: 384  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 324  
; LENGTH: 1619  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-388-360-324

Alignment Scores:  
Pred. No.: 1,04e-92 Length: 1619  
Score: 778.00 Matches: 142  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 15 Gaps: 0

US-09-690-825-34 (1-142) x US-10-388-360-324 (1-1619)

QY 1 MetGlyAlaProThrLeuProProAlaTTPGlnProPheLeuYsAspHisArgIleSer 20  
Db 50 ATGGGTGCCCCGACGCTTGCCCTTCTGCAAGACACCGCATCTCT 109

QY 21 ThrpheylsAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40  
Db 110 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGCGCCCTGCACCCCGAGCGGATGGCCGAG 169  
QY 41 AlaglyPheIleHIScysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60  
Db 170 GCTGGCTTCATCCACTGCCCTCCACTGAGACAGCACTGGCCGAGGTTCTTCTTCTGC 229  
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspAspProIleGluGluHISLysLysHIS 80  
Db 230 TTCAAGAGAGCTGGAAGCTGGAGCCAGATGACGACCCCATAGAGGAACTATAAAGCAT 289  
QY 81 SerSerGlyCysAlaPheLeuSerValLysGlnPheGluGluLeuThrLeuGlyGlu 100  
Db 290 TCGTCGGGTTCGCTTCTTCTTCTGTCAGAGAGCATTTGAAAGATTAAACCTTGTGTGA 349  
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120  
Db 350 TTTTGAACCTGCACAGAGAAAGCCAGAACAAATTGCAGAGAAACCAACAACTAAG 409  
QY 121 LysLysGluPheGluGluThrAlaLysValArgArgAlaIleGluGlnLeuAlaAla 140  
Db 410 AAGAAAGAAATTGAGAAACTGCGAAGAAAGTGCCTGCATCGACGAGCTGCTGCC 469  
QY 141 MetAsp 142  
Db 470 ATGGAT 475

## RESULT 5

US-10-342-887-566  
Sequence 566, Application US/10342887  
Publication No. US20040058340A1  
GENERAL INFORMATION:  
APPLICANT: Dai, Hongyue  
APPLICANT: He, Jindong  
APPLICANT: Linsley, Peter S.  
APPLICANT: Mao, Mao  
APPLICANT: Roberts, Christopher J.  
APPLICANT: Van 't Veer, Laura Johanna  
APPLICANT: Van de Vijver, Marc J.  
APPLICANT: Bernards, Rene  
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients  
FILE REFERENCE: 9301-188-999  
CURRENT APPLICATION NUMBER: US/10/342,887  
CURRENT FILING DATE: 2003-01-15  
PRIOR APPLICATION NUMBER: 60/298,918  
PRIOR FILING DATE: 2001-06-18  
PRIOR APPLICATION NUMBER: 60/380,710  
PRIOR FILING DATE: 2002-05-14  
PRIOR APPLICATION NUMBER: 10/172,118  
PRIOR FILING DATE: 2002-06-14  
NUMBER OF SEQ ID NOS: 2699  
SEQ ID NO 566  
LENGTH: 1619  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-342-887-566

## Alignment Scores:

Pred. No.: 1,04e-92 Length: 1619  
Score: 778.00 Matches: 142  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 16 Gaps: 0

US-09-690-825-34 (1-142) x US-10-342-887-566 (1-1619)

QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20  
Db 50 ATGGGTGCCCCGAGCTGGCCCTGCTGCGACGCCCTTTCTCAAGGACCAACCGCATCTCT 109

QY 21 ThrpheylsAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40  
Db 110 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGCGCCCTGCACCCCGAGCGGATGGCCGAG 169  
QY 41 AlaglyPheIleHIScysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60  
Db 170 GCTGGCTTCATCCACTGCCCTCCACTGAGACAGCACTGGCCGAGGTTCTTCTTCTGC 229  
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspAspProIleGluGluHISLysLysHIS 80  
Db 230 TTCAAGAGAGCTGGAAGCTGGAGCCAGATGACGACCCCATAGAGGAACTATAAAGCAT 289  
QY 81 SerSerGlyCysAlaPheLeuSerValLysGlnPheGluGluLeuThrLeuGlyGlu 100  
Db 290 TCGTCGGGTTCGCTTCTTCTTCTGTCAGAGAGCATTTGAAAGATTAAACCTTGTGTGA 349  
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120  
Db 350 TTTTGAACCTGCACAGAGAAAGCCAGAACAAATTGCAGAGAAACCAACAACTAAG 409  
QY 121 LysLysGluPheGluGluThrAlaLysValArgArgAlaIleGluGlnLeuAlaAla 140  
Db 410 AAGAAAGAAATTGAGAAACTGCGAAGAAAGTGCCTGCATCGACGAGCTGCTGCC 469  
QY 141 MetAsp 142  
Db 470 ATGGAT 475

## RESULT 7

US-10-283-975A-445  
Sequence 445, Application US/10283975A  
Publication No. US20040110792A1  
GENERAL INFORMATION:  
APPLICANT: Ortho-Clinical Diagnostics, Inc.  
TITLE OF INVENTION: Methods for Assessing and Treating Leukemia  
FILE REFERENCE: CDS 293 PCT  
CURRENT APPLICATION NUMBER: US/10/283,975A  
CURRENT FILING DATE: 2002-10-30  
PRIOR APPLICATION NUMBER: 60/340,938  
PRIOR FILING DATE: 2001-10-30  
PRIOR APPLICATION NUMBER: 60/338,997  
PRIOR FILING DATE: 2001-10-30  
PRIOR APPLICATION NUMBER: 60/340,081  
PRIOR FILING DATE: 2001-10-30  
PRIOR APPLICATION NUMBER: 60/341,012  
PRIOR FILING DATE: 2001-10-30  
NUMBER OF SEQ ID NOS: 900  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 445  
LENGTH: 1619  
TYPE: DNA  
ORGANISM: HUMAN  
US-10-283-975A-445

## Alignment Scores:

Pred. No.: 1,04e-92 Length: 1619  
Score: 778.00 Matches: 142  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 17 Gaps: 0

US-09-690-825-34 (1-142) x US-10-283-975A-445 (1-1619)

QY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20  
Db 50 ATGGGTGCCCCGAGCTGGCCCTGCTGCGACGCCCTTTCTCAAGGACCAACCGCATCTCT 109  
QY 21 ThrpheylsAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40  
Db 110 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGCGCCCTGCACCCCGAGCGGATGGCCGAG 169  
QY 41 AlaglyPheIleHIScysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60

```
Db 170 GGTGGTTTATCCACGCCCCCTGAGAACGAGCAAGATTGGCCAGTGTCTTCTGCG 229
Qy 61 PheLysGluLeuGluGlyTTPGluProAspAspProIleGluGluHis 80
Db 230 TTCAGAGACTGGAGGCTGGAGCCAGATGACAGCCCATAGAGAACATTAAGCAT 289
Qy 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
Db 290 TCGTCGGGTGGCTTCTCTCTCTGTCAGAAAGCAGTTTGAAGAAATTAACTTGTGTGA 349
Qy 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
Db 350 TTTTGAAGACTGGACAGAGAAAGCCAGAACAAATTGCAAGAGAACCAACATTAAG 409
Qy 121 LysLysGluPheGluGluGluThrAlaLysLysValArgArgAlaIleGluGluLeuAla 140
Db 410 AAGAAAGAAATTGAGAGAACTGGAGAGAAAGTGGCCCTGCGCATCGAGCAGCTGGCTGCC 469
Qy 141 MetAsp 142
Db 470 ATGGAT 475

RESULT 8
US-10-657-022-99
; Sequence 99, Application US/10657022
; Publication No. US20040180354A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Liu, Liping
; APPLICANT: Liu, Zheng
; TITLE OF INVENTION: EPIPOPE SEQUENCES
; FILE REFERENCE: MANK 032A
; CURRENT APPLICATION NUMBER: US/10/657, 022
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: 60/409123
; PRIOR FILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 610
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 99
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-657-022-99

Alignment Scores:
Pred. No.: 1.04e-92 Length: 1619
Score: 778.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-690-825-34 (1-142) x US-10-657-022-99 (1-1619)
Qy 1 MetGlyAlaProThrLeuProProAlaTTPGlnProPheLeuLysAspHisArgIleSer 20
Db 50 ATGGGTGCCCCGAGCTTGGCCCTGCTGAGCGCTTCTTCAAGGACCCCATCTCT 109
Qy 21 ThrPheLysAsnTTPProPheLeuGluGlyCysAlaGlyThrProGluArgMetAlaGlu 40
Db 110 ACATTCAAGAGCTGGCCCTTCTTGGAGGCTGGCGCTGCAACCCCGAGCGGATGGCCGAG 169
Qy 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
Db 170 GCTGGCTTCACTCCATCCCTCCCATCGAGACGAGCAACTGGCCCGCATGTTCTTCTGCG 229
Qy 61 PheLysGluLeuGluGlyTTPGluProAspAspAspProIleGluGluHis 80
Db 230 TTCAGAGAGCTGGAGGCTGGAGCCAGATGACAGCCCATAGAGGAACATTAAGCAT 289
Qy 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
```

```
Db 290 TCGTCGGGTGGCTTCTCTCTCTGTCAGAAAGCAGTTTGAAGAAATTAACTTGTGTGA 349
Qy 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
Db 350 TTTTGAAGACTGGACAGAGAAAGCCAGAACAAATTGCAAGAGAACCAACATTAAG 409
Qy 121 LysLysGluPheGluGluGluThrAlaLysLysValArgArgAlaIleGluGluLeuAla 140
Db 410 AAGAAAGAAATTGAGAGAACTGGAGAGAAAGTGGCCCTGCGCATCGAGCAGCTGGCTGCC 469
Qy 141 MetAsp 142
Db 470 ATGGAT 475

RESULT 9
US-10-807-897-1
; Sequence 1, Application US/10807897
; Publication No. US20040192631A1
; GENERAL INFORMATION:
; APPLICANT: Xiang, Rong
; APPLICANT: Zhou, He
; APPLICANT: Reisfeld, Ralph A.
; TITLE OF INVENTION: The Scripts Research Institute
; TITLE OF INVENTION: DNA VACCINES AGAINST TUMOR GROWTH AND
; FILE REFERENCE: TSRI-874.1
; CURRENT APPLICATION NUMBER: US/10/807, 897
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457, 009
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
; US-10-807-897-1

Alignment Scores:
Pred. No.: 1.06e-92 Length: 1643
Score: 778.00 Matches: 142
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-690-825-34 (1-142) x US-10-807-897-1 (1-1643)
Qy 1 MetGlyAlaProThrLeuProProAlaTTPGlnProPheLeuLysAspHisArgIleSer 20
Db 45 ATGGGTGCCCCGAGCTTGGCCCTGCTGAGCGCTTCTTCAAGAGCCCATCTCT 104
Qy 21 ThrPheLysAsnTTPProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db 105 ACATTCAAGAGCTGGCCCTTCTTGGAGGCTGGCGCTGCAACCCCGAGCGGATGGCCGAG 164
Qy 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
Db 165 GCTGGCTTCACTCCATCCCTCCCATCGAGACGAGCACTTGGCCCGCATGTTCTTCTGCG 224
Qy 61 PheLysGluLeuGluGlyTTPGluProAspAspAspProIleGluGluHis 80
Db 225 TTCAGAGACTGGAGGCTGGAGCCAGATGACAGCCCATAGAGAACATTAAGCAT 284
Qy 81 SerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluGluLeuThrLeuGlyGlu 100
Db 285 TCGTCGGGTGGCTTCTCTCTCTGTCAGAAAGCAGTTTGAAGAAATTAACTTGTGTGA 344
Qy 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnAsnLys 120
Db 345 TTTTGAAGACTGGACAGAGAAAGCCAGAACAAATTGCAAGAGAACCAACATTAAG 404
```

OY 121 LysylsglupehgiugluThralalysylsValargalallegiugluLeuAla140  
Db 405 AAGAAAGATTGTGAGAAAGTGCAGAAAGTGGCCCTGTCAGACGCTGGCTGCC 464  
OY 141 Metasp 142  
Db 465 ATGGAT 470

## RESULT 10

US-10-071-766-109  
; Sequence 109, Application US/10071766  
; Publication No. US20020192678A1  
; GENERAL INFORMATION:  
; APPLICANT: Huel-Mei Chen  
; TITLE OF INVENTION: GENES EXPRESSED IN SENESENCE  
; FILE REFERENCE: PA-0043 US  
; CURRENT APPLICATION NUMBER: US/10/071,766  
; CURRENT FILING DATE: 2002-02-07  
; NUMBER OF SEQ ID NOS: 144  
; SOFTWARE: PERL Program  
; SEQ ID NO: 109  
; LENGTH: 2404  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Inbyte ID No. US20020192678A1 251651.4  
; NAME/KEY: unsure  
; LOCATION: 710, 717, 724, 982-1007  
; OTHER INFORMATION: a, t, c, g, or other  
US-10-071-766-109

## Alignment Scores:

Pred. No.: 1,78e-92 Length: 2404  
Score: 778.00 Matches: 142  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 13 Gaps: 0

US-09-690-825-34 (1-142) x US-10-071-766-109 (1-2404)

OY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20  
Db 56 ATGGTGCCCCGAGCGTGGCCCCCTGGCTGGCAGCCCTTCTCAAGGACCCACCATCTCT 115  
OY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40  
Db 116 ACATTCAAGAACTGGCCCTTCTTGGAGGCTGGCGCTGCACCCCGAGCGGATGGCCGAG 175  
OY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60  
Db 176 GCTGGCTTCATCCACTGCCCCACGAGAACGAGCCAGACTTGGCCCAAGTCTTCTCTGC 235  
OY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHis 80  
Db 236 TTCAAGAGCTGGAAGGCTGGAGCCGAGATGACGACCCCATAGAGAACTAAAGACAT 295  
OY 81 SerSerGlyCysAlaPheLeuSerValIleLysGlnPheGluGluLeuThrLeuGlyGlu 100  
Db 296 TCGTCCGCTTGGCTTCTTCTTCTGTCAGAGACAGTTTGAAGATTAACCTTGGTGA 355  
OY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120  
Db 356 TTTTGGAACTGGGACAGAGAAAGGCCAGAACAAATTGCAAGAAACCAACATAAG 415  
OY 121 LysylsglupehgiugluThralalysylsValargalallegiugluLeuAla140  
Db 416 AAGAAAGATTGTGAGAAAGTGCAGAAAGTGGCCCTGTCAGACGCTGGCTGCC 475  
OY 141 Metasp 142  
Db 476 ATGGAT 481

## RESULT 11

US-10-084-817-285  
; Sequence 285, Application US/10084817  
; Publication No. US20030119009A1  
; GENERAL INFORMATION:  
; APPLICANT: Susan Stuart  
; APPLICANT: Jed G. Nuchtern  
; APPLICANT: Sharon E. Plon  
; APPLICANT: Jason M. Shohet  
; TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION  
; FILE REFERENCE: PA-0046 US  
; CURRENT APPLICATION NUMBER: US/10/084,817  
; CURRENT FILING DATE: 2002-02-25  
; PRIOR APPLICATION NUMBER: 60/270,784  
; PRIOR FILING DATE: 2001-02-23  
; NUMBER OF SEQ ID NOS: 365  
; SOFTWARE: PERL Program  
; SEQ ID NO: 285  
; LENGTH: 2404  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Inbyte ID No. US20030119009A1 251651.4  
; NAME/KEY: unsure  
; LOCATION: 710, 717, 724  
; OTHER INFORMATION: a, t, c, g, or other  
US-10-084-817-285

## Alignment Scores:

Pred. No.: 1,78e-92 Length: 2404  
Score: 778.00 Matches: 142  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 15 Gaps: 0

US-09-690-825-34 (1-142) x US-10-084-817-285 (1-2404)

OY 1 MetGlyAlaProThrLeuProProAlaTrpGlnProPheLeuLysAspHisArgIleSer 20  
Db 56 ATGGTGCCCCGAGCGTGGCCCCCTGGCTGGCAGCCCTTCTCAAGGACCCACCATCTCT 115  
OY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40  
Db 116 ACATTCAAGAACTGGCCCTTCTTGGAGGCTGGCGCTGCACCCCGAGCGGATGGCCGAG 175  
OY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60  
Db 176 GCTGGCTTCATCCACTGCCCCACGAGAACGAGCCAGACTTGGCCCAAGTCTTCTCTGC 235  
OY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHis 80  
Db 236 TTCAAGAGCTGGAAGGCTGGAGCCGAGATGACGACCCCATAGAGAACTAAAGACAT 295  
OY 81 SerSerGlyCysAlaPheLeuSerValIleLysGlnPheGluGluLeuThrLeuGlyGlu 100  
Db 296 TCGTCCGCTTGGCTTCTTCTTCTGTCAGAGACAGTTTGAAGATTAACCTTGGTGA 355  
OY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120  
Db 356 TTTTGGAACTGGGACAGAGAAAGGCCAGAACAAATTGCAAGAAACCAACATAAG 415  
OY 121 LysylsglupehgiugluThralalysylsValargalallegiugluLeuAla140  
Db 416 AAGAAAGATTGTGAGAAAGTGCAGAAAGTGGCCCTGTCAGACGCTGGCTGCC 475  
OY 141 Metasp 142  
Db 476 ATGGAT 481

RESULT 12



```

US-10-741-601-210
; Sequence 210, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/10/741,601
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 210
; LENGTH: 2570
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-601-210

Alignment Scores:
Pred. No.: 1,228-91      Length: 2570
Score: 772.00           Matches: 141
Percent Similarity: 99.30%  Conservative: 0
Best Local Similarity: 99.30%  Mismatches: 1
Query Match: 99.23%      Indels: 0
DB: 17                  Gaps: 0

US-09-690-825-34 (1-142) x US-10-741-601-210 (1-2570)
QY 1 MetGlyAlaProThrLeuProProAlaTTPGlnProPheLeuLysAspHisArgIleSer 20
Db 75 ATGGGTGCCCCGACGCTTGCCCTGCTGCGACGCCCTTCTCAAGACCAACCGCATCTCT 134
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db 135 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGGCGCTGCACCCCGAGCGATGGCCGAG 194
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
Db 195 GCTGGCTTCATCCACTGCCCTGAGAACGAGCCGACTGGCCCGCAGTTCCTTCTTGC 254
QY 61 PheLeuGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis 80
Db 255 TTCAAGAGCTGGAAGCTGGAGCCAGATGACGACCCCATAGAGAAACATATAAAGCAT 314
QY 81 SerSerGlyCysAlaPheLeuSerValLysGlnPheGluLeuThrLeuGlyGlu 100
Db 315 TCGTCCGGTGGCCCTTCTTCTGTCAGAAAGCATTTGAAGATTAAACCTTGGTGA 374
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
Db 375 TTTTGAACCTGACAGAGAAAGCCCAAGACAAATTGCAAGAAACCAACATAAG 434
QY 121 LysLysGluPheGluGluGluThrAlaLysValArgArgAlaIleGluGluLeuAla 140
Db 435 AAGAAGAAATTGAGAGAACTGCGRAGAAAGTGGCGCTGCCATCGACGAGCTGGCC 494
QY 141 MetAsp 142
Db 495 ATGGAT 500

RESULT 13
US-10-741-601-216
; Sequence 216, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/10/741,601
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 216
; LENGTH: 2570
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-601-216

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; SEQ ID NO 216
; LENGTH: 2585
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-601-216

Alignment Scores:
Pred. No.: 1,238-91      Length: 2585
Score: 772.00           Matches: 141
Percent Similarity: 99.30%  Conservative: 0
Best Local Similarity: 99.30%  Mismatches: 1
Query Match: 99.23%      Indels: 0
DB: 17                  Gaps: 0

US-09-690-825-34 (1-142) x US-10-741-601-216 (1-2585)
QY 1 MetGlyAlaProThrLeuProProAlaTTPGlnProPheLeuLysAspHisArgIleSer 20
Db 75 ATGGGTGCCCCGACGCTTGCCCTGCTGCGACGCCCTTCTCAAGACCAACCGCATCTCT 134
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40
Db 135 ACATTCAAGAACTGGCCCTTCTTGAGGGCTGGCGCTGCACCCCGAGCGATGGCCGAG 194
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60
Db 195 GCTGGCTTCATCCACTGCCCTGAGAACGAGCCGACTTGCCCGCAGTTCCTTCTTGC 254
QY 61 PheLysGluLeuGluGlyTrpGluProAspAspProIleGluGluHisLysLysHis 80
Db 255 TTCAAGAGCTGGAAGCTGGAGCCAGATGACGACCCCATAGAGAAACATATAAAGCAT 314
QY 81 SerSerGlyCysAlaPheLeuSerValLysGlnPheGluGluLeuThrLeuGlyGlu 100
Db 315 TCGTCCGGTGGCTTCTTCTTCTGTCAGAAAGCATTTGAAGATTAAACCTTGGTGA 374
QY 101 PheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThrAsnLys 120
Db 375 TTTTGAACCTGACAGAGAAAGCCCAAGACAAATTGCAAGAAACCAACATAAG 434
QY 121 LysLysGluPheGluGluGluThrAlaLysValArgArgAlaIleGluGluLeuAla 140
Db 435 AAGAAGAAATTGAGAGAACTGCGRAGAAAGTGGCGCTGCCATCGACGAGCTGGCC 494
QY 141 MetAsp 142
Db 495 ATGGAT 500

RESULT 14
US-10-741-601-215
; Sequence 215, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/10/741,601
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 215
; LENGTH: 2639
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-601-215

Alignment Scores:
Pred. No.: 8,98-89      Length: 2639
Score: 750.50           Matches: 141
Percent Similarity: 85.45%  Conservative: 0
Best Local Similarity: 85.45%  Mismatches: 1
Query Match: 96.47%      Indels: 23

```

DB: 17 Gaps: 1  
US-09-690-825-34 (1-142) x US-10-741-601-215 (1-2639)  
QY 1 MetGlyAlaProThrLeuProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 20  
DB 75 ATGGGTGCGCCGAGCGTTGCGCCCTGCGGAGCCCTTCTCAAGGACCAACCGCATCTCT 134  
QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40  
DB 135 ACATTCAAGAACTGGCCCTTCTTGAGAGGCTGCGCCCTGCAACCCCGAGCGGATGGCCGAG 194  
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60  
DB 195 GCTGGCTTCATCCACTGCGCCCGCAGACGAGCAACCTTGGCCCGCATGTTCTTCTTCTGCG 254  
QY 61 PheLysGluLeuGluGlyTTPGluProAspAspProIle----- 74  
DB 255 TTCAGAGAGCTGGAGGCTGGAGCCAGATGACGCCATTTGGCCGCGGACAGCTGGCT 314  
QY 75 -----GluGluHis 77  
DB 315 TACGCTGTAAATACAGACACTTTGGAGCGCGGCGGATCAGAGAGAGAACT 374  
QY 78 LysLysHisSerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluLeuThr 97  
DB 375 AAAAAGCAATTCGTCGCGTGGCTTCTTCTGTCAAGAGCAGATTGAAGATTAAAC 434  
QY 98 LeuGlyGluPheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThr 117  
DB 435 CTGGTGAATTTTGAACCTGACAGAGAAAGACCAGAACAAATTGCAAGGAAACC 494  
QY 118 AsnAsnLysLysLysGluPheGluGluThrAlaLysLysValaArgAlaIleGluGln 137  
DB 495 AACAAATAGAGAAAGAAATTGAGGAAACTGCGRAGAAATGCGCGCTGCATCGAGCAG 554  
QY 138 LeuAlaAlaMetAsp 142  
DB 555 CTGGCTGCCATGAGT 569  
RESULT 15  
US-10-741-601-211  
; Sequence 211, Application US/10741601  
; Publication No. US20040166519A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGIL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO01500  
; CURRENT APPLICATION NUMBER: US/10/741.601  
; NUMBER OF SEQ ID NOS: 26415  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 211  
; LENGTH: 2654  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-741-601-211  
Alignment Scores:  
Pred. No.: 8,97e-89 Length: 2654  
Score: 750.50 Matches: 141  
Percent Similarity: 85.45% Conservative: 0  
Best Local Similarity: 85.45% Mismatches: 1  
Query Match: 96.47% Indels: 23  
DB: 17 Gaps: 1  
US-09-690-825-34 (1-142) x US-10-741-601-211 (1-2654)  
QY 1 MetGlyAlaProThrLeuProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 20  
DB 75 ATGGGTGCGCCGAGCGTTGCGCCCTGCGGAGCCCTTCTCAAGGACCAACCGCATCTCT 134

QY 21 ThrPheLysAsnTrpProPheLeuGluGlyCysAlaCysThrProGluArgMetAlaGlu 40  
DB 135 ACATTCAAGAACTGGCCCTTCTTGAGAGGCTGCGCCCTGCAACCCCGAGCGGATGGCCGAG 194  
QY 41 AlaGlyPheIleHisCysProThrGluAsnGluProAspLeuAlaGlnCysPhePheCys 60  
DB 195 GCTGGCTTCATCCACTGCGCCCGCAGACGAGCAACCTTGGCCCGCATGTTCTTCTTCTGCG 254  
QY 61 PheLysGluLeuGluGlyTTPGluProAspAspProIle----- 74  
DB 255 TTCAGAGAGCTGGAGGCTGGAGCCAGATGACGCCATTTGGCCGCGGACAGCTGGCT 314  
QY 75 -----GluGluHis 77  
DB 315 TACGCTGTAAATACAGACACTTTGGAGCGCGGCGGATCAGAGAGAGAACT 374  
QY 78 LysLysHisSerSerGlyCysAlaPheLeuSerValLysLysGlnPheGluLeuThr 97  
DB 375 AAAAAGCAATTCGTCGCGTGGCTTCTTCTGTCAAGAGCAGATTGAAGATTAAAC 434  
QY 98 LeuGlyGluPheLeuLysLeuAspArgGluArgAlaLysAsnLysIleAlaLysGluThr 117  
DB 435 CTGGTGAATTTTGAACCTGACAGAGAAAGACCAGAACAAATTGCAAGGAAACC 494  
QY 118 AsnAsnLysLysLysGluPheGluGluThrAlaLysLysValaArgAlaIleGluGln 137  
DB 495 AACAAATAGAGAAAGAAATTGAGGAAACTGCGRAGAAATGCGCGCTGCATCGAGCAG 554  
QY 138 LeuAlaAlaMetAsp 142  
DB 555 CTGGCTGCCATGAGT 569

Search completed: November 1, 2004, 20:32:08  
Job time : 376 secs